

SEQUENCE LISTING

<110> O'Donnell, Michael E.
 Yuzhakov, Alexander
 Yurieva, Olga
 Jeruzalmi, David
 Bruck, Irina
 Kuriyan, John

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
 FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
 USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 60/143,202

<151> 1997-04-08

<150> 08/823,407

<151> 1997-04-08

<150> 09/057,416

<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

<210> 1

<211> 2007

<212> DNA

<213> *Thermus thermophilus*

<400> 1

```
tccggggggtg gggttcccag gtagaccocg gccctcccg tgagcccctt taccaggcc 60
gccacctcct ccaggggggc caaggcgtgc aaggagagga acgtccgcac cacgccctat 120
actagccttg tgagcgccct ctaccgccgc ttccgcccc tcacctcca ggaggtggtg 180
gggcaggagc acgtgaagga gccctcctc aaggccatcc gggaggggag gctcgcccag 240
gcctacctct tctccgggcc caggggcgtg ggcaagacca ccacggcgag gtcctcgcc 300
atggcggtgg ggtgccaggg ggaagacccc ccttgcgggg tctgccccca ctgccaggcg 360
gtgcagaggg gcgcccaccc ggacgtggtg gacattgacg ccgccagcaa caactccgtg 420
gaggacgtgc gggagctgag ggaaaggatc cacctcgccc ccctctctgc cccaggaag 480
gtcttcatcc tggacgagge ccacatgctc tccaaaagcg ccttcaacgc cctcctcaag 540
accctggagg agccccgcgc ccacgtcctc ttcgctcttcg ccaccacga gcccgagagg 600
atgcccccca ccacctctc ccgcacccag cacttccgct tccgccgcct cacggaggag 660
```

```

gagatcgctt ttaagctccg ggcgcctcctg gagggccgtgg ggcggggaggc ggaggaggag 720
gccctcctcc tcctcgcccc cctggcgaggc gggggccctta gggacgcgga aagcctcctg 780
gagcgcttcc tcctcctgga agggcccccctc acccggaagg aggtggagcg cgccctaggc 840
tcccccccag ggaccgggggt ggccgagatc gccgcctccc tcgcgagggg gaaaacggcg 900
gaggccctgg gcctcgcccc ggcgcctctac ggggaaggggt acgccccgag gagcctgggtc 960
tcgggccttt tggaggtggt ccgggaaggc ctctacgccg ccttcggcct cgcggaacc 1020
ccccttcccc ccccgcccca ggccctgatc gccgccatga ccgccctgga cgaggccatg 1080
gagcgctcgc ccgcgcgctc cgacgcctta agcctggagg tggccctcct ggaggcgga 1140
agggccctgg ccgcccaggc cctaccccag ccacggggcg ctccctcccc agaggtcggc 1200
cccaagccgg aaagcccccc gaccccggaa ccccaaggc ccgaggaggc gcccgcctg 1260
cgggagcggt ggcgggcctt cctcgaggcc ctccaggcca ccctacgggc cttcgtgcgg 1320
gaggcccgcc cggaggtccg ggaaggccag ctctgcctcg ctttccccga ggacaaggcc 1380
ttccactacc gcaaggcctc ggaacagaag gtgaggctcc tccccctggc ccaggcccat 1440
ttcgggggtg aggaggtcgt cctcgtcctg gagggagaaa aaaaaagcct gagcccaagg 1500
ccccgcccgg ccccacctcc tgaagcgccc gcacccccgg gccctcccga ggaggaggta 1560
gaggcggagg aagcggcgga ggaggccccg gaggaggcct tgaggcggtt ggtccgcctc 1620
ctggggggggc ggggtgctct ggtgcggcgcc ccaggagccc gggaggcgcc ggaggaggaa 1680
cccctgagcc aagacgagat aggggggtact ggtatataat gggggcatga cgcggaccac 1740
cgacctcgga caagagaccg tggacaacat cctcaagcgc ctccgccgta ttgaggcca 1800
ggtgcggggg ctccagaaga tggtgggcca gggccgcccc tgcgacgagg tcctcaccca 1860
gatgaccgcc accaagaagg ccatggaggc ggcggccacc ctgatcctcc acgagttcct 1920
gaacgtctgc gccgcccagg tctccgaggg caaggtgaac cccaagaagc ccgaggagat 1980
cgccaccatg ctgaagaact tcattcta 2007

```

<210> 2

<211> 529

<212> PRT

<213> *Thermus thermophilus*

<400> 2

Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
1				5					10					15	

Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
			20					25						30	

Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
		35					40					45			

Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
	50					55					60				

Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
65					70					75					80

Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
				85				90						95	

Val	Glu	Asp	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ile	His	Leu	Ala	Pro	Leu		
			100					105					110				
Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser		
		115					120					125					
Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro		
	130					135					140						
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro		
145					150					155					160		
Thr	Ile	Leu	Ser	Arg	Thr	Gln	His	Phe	Arg	Phe	Arg	Arg	Leu	Thr	Glu		
				165					170					175			
Glu	Glu	Ile	Ala	Phe	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ala	Val	Gly	Arg		
			180					185					190				
Glu	Ala	Glu	Glu	Glu	Ala	Leu	Leu	Leu	Leu	Ala	Arg	Leu	Ala	Asp	Gly		
		195					200					205					
Ala	Leu	Arg	Asp	Ala	Glu	Ser	Leu	Leu	Glu	Arg	Phe	Leu	Leu	Leu	Glu		
		210				215					220						
Gly	Pro	Leu	Thr	Arg	Lys	Glu	Val	Glu	Arg	Ala	Leu	Gly	Ser	Pro	Pro		
225					230					235					240		
Gly	Thr	Gly	Val	Ala	Glu	Ile	Ala	Ala	Ser	Leu	Ala	Arg	Gly	Lys	Thr		
				245					250					255			
Ala	Glu	Ala	Leu	Gly	Leu	Ala	Arg	Arg	Leu	Tyr	Gly	Glu	Gly	Tyr	Ala		
			260					265					270				
Pro	Arg	Ser	Leu	Val	Ser	Gly	Leu	Leu	Glu	Val	Phe	Arg	Glu	Gly	Leu		
		275					280					285					
Tyr	Ala	Ala	Phe	Gly	Leu	Ala	Gly	Thr	Pro	Leu	Pro	Ala	Pro	Pro	Gln		
	290					295					300						
Ala	Leu	Ile	Ala	Ala	Met	Thr	Ala	Leu	Asp	Glu	Ala	Met	Glu	Arg	Leu		
305					310					315					320		
Ala	Arg	Arg	Ser	Asp	Ala	Leu	Ser	Leu	Glu	Val	Ala	Leu	Leu	Glu	Ala		
				325					330					335			
Gly	Arg	Ala	Leu	Ala	Ala	Glu	Ala	Leu	Pro	Gln	Pro	Thr	Gly	Ala	Pro		
			340					345					350				

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445

Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
 450 455 460

Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu
 465 470 475 480

Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
 485 490 495

Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
 500 505 510

Ala Pro Glu Glu Glu Pro Leu Ser Gln Asp Glu Ile Gly Gly Thr Gly
 515 520 525

Ile

<210> 3

<211> 1590

<212> DNA

<213> Thermus thermophilus

<400> 3

gtgagcgccc tctaccgccg cttccgcccc ctcaccttcc aggaggtggt ggggcaggag 60
 cacgtgaagg agcccctcct caaggccatc cgggagggga ggctcgccca ggcctacctc 120
 ttctccgggc ccagggggtt gggcaagacc accacggcga ggctcctcgc catggcggtg 180
 ggggtgccagg gggaagaccc cccttgcggtg gtctgcccc actgccaggc ggtgcagagg 240


```

ggcgcccacc cggacgtggt ggacattgac gccgccagca acaactccgt ggaggacgtg 300
cgggagctga gggaaaggat ccacctcgcc cccctctctg ccccaggaa ggtcttcac 360
ctggacgagg cccacatgct ctccaaaagc gccttcaacg cctcctcaa gacctggag 420
gagccccgcg cccacgtcct ctctgtcttc gccaccaccg agcccgagag gatgcccccc 480
accatcctct cccgcaccca gcacttcgcg ttccgccgcc tcacggagga ggagatcgcc 540
tttaagctcc ggcgcacccg ggaggccgtg gggcgaggag cggaggagga ggccctcctc 600
ctcctcgccc gcctggcgga cggggccctt agggacgcgg aaagcctcct ggagcgcttc 660
ctcctcctgg aaggccccct cacccggaag gaggtggagc gcgccttagg ctcccccca 720
gggaccgggg tggccgagat cgcgcctcc ctcgcgaggg ggaaaacggc ggaggccctg 780
ggcctcgccc ggcgcctcta cggggaaggg tacgccccga ggagcctggt ctcgggcctt 840
ttggaggtgt tccgggaagg cctctacgcc gccttcggcc tcgcgggaac ccccttccc 900
gccccgcccc aggcctgat cgcgcctatg accgccttg acgaggccat ggagcgcttc 960
gccccgcgct ccgacgcctt aagcctggag gtggccctcc tggaggcggg aaggccctg 1020
gccgccgagg ccctaccca gccacgggc gctccttccc cagaggtcgg cccaagccg 1080
gaaagcccc cgaacccgga accccaagg cccgaggagg cgcgcgacct gcgggagcgg 1140
tggcgggcct tctcgaggc cctcaggccc accctacggg ccttcgtgcg ggaggcccgc 1200
ccggaggtcc gggaaggcca gctctgcctc gctttccccg aggacaaggc cttccactac 1260
cgcaaggcct cggaacagaa ggtgaggctc ctccccctgg ccaggccca tttcggggtg 1320
gaggaggtcg tctcgtcct ggagggagaa aaaaaaagcc tgagcccaag gccccgcccg 1380
gccccacctc ctgaagcgcc cgcacccccg ggccctcccg aggaggaggt agaggcggag 1440
gaagcggcgg aggaggcccc ggaggaggcc ttgaggcggg tggtcgcct cctggggggg 1500
cgggtgctct ggggtgcggc gccaggacc cgggaggcgc cggaggagga acccctgagc 1560
caagacgaga taggggttac tggtatataa 1590

```

<210> 4

<211> 464

<212> PRT

<213> *Thermus thermophilus*

<400> 4

```

Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1              5              10              15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
          20              25              30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
          35              40              45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
          50              55              60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
          65              70              75              80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
          85              90              95

```

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
 290 295 300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 305 310 315 320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365
 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430
 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445
 Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser
 450 455 460

<210> 5
 <211> 454
 <212> PRT
 <213> Thermus thermophilus

<400> 5
 Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser

85

90

95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
 290 295 300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 305 310 315 320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro

340	345	350
Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro		
355	360	365
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe		
370	375	380
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg		
385	390	400
Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys		
405	410	415
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro		
420	425	430
Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu		
435	440	445
Gly Glu Lys Lys Lys Ala		
450		

<210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 6
 cgcaagcttc acgcstacct sttctccggs ac

32

<210> 7
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 7
 His Ala Tyr Leu Phe Ser Gly Thr
 1 5

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
cgcggaattcg tgctcsggsg gctcctcsag sgtc 34

<210> 9
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 9
Lys Thr Leu Glu Glu Pro Pro Glu His
1 5

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
gcgcggatcc ggagggagaa aaaaaaagcc tcagccca 38

<210> 11
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
gcgcggatcc ggagggagag aagaaaagcc tcagccca 38

<210> 12
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 12
 gaattaaatt cgcgcttcgg gaggtggg 28

 <210> 13
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 13
 gcgcgaattc gcgcttcggg aggtggg 27

 <210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 14
 gcgcgaattc gggcgcttca ggaggtggg 29

 <210> 15
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 15
 gtggtgcata tggtgagcgc cctctaccgc c 31

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
gtggtggtcg acccaggagg gccacctcca g

31

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (2)
<223> X is any aa at position 2

<220>
<221> PEPTIDE
<222> (3)
<223> X is any aa at position 3

<220>
<221> PEPTIDE
<222> (5)
<223> X is any aa at position 5

<400> 17
Gly Xaa Xaa Gly Xaa Gly Lys Thr
1 5

<210> 18
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 18

Lys Pro Asp Pro Lys Ala Pro Pro Gly Pro Thr Ser
1 5 10

<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val
180

```
<400> 20
Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
  1             5             10             15
```

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
65 70 75 80

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
100 105 110

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
165 170 175

<210>	21
<211>	294
<212>	PRT

<213> Escherichia coli

<400> 21

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn
180 185 190

Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg
195 200 205

Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met
225 230 235 240

Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met
 245 250 255
 Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala
 260 265 270
 Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu
 275 280 285
 Leu His Arg Ile Ala Met
 290
 <210> 22
 <211> 294
 <212> PRT
 <213> Haemophilus influenzae
 <400> 22
 Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
 1 5 10 15
 Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
 20 25 30
 Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
 35 40 45
 Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
 50 55 60
 Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
 65 70 75 80
 Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
 85 90 95
 Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
 100 105 110
 Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
 115 120 125
 His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
 130 135 140
 Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
 145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
225 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
275 280 285

Leu His Gln Ile Ala Leu
290

<210> 23
<211> 294
<212> PRT
<213> Bacillus subtilis

<400> 23
Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65	70	75	80
Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala			
85	90	95	
Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys			
100	105	110	
Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val			
115	120	125	
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu			
130	135	140	
Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His			
145	150	155	160
Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys			
165	170	175	
Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp			
180	185	190	
Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser			
195	200	205	
Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala			
210	215	220	
Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile			
225	230	235	240
Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu			
245	250	255	
His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu			
260	265	270	
Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr			
275	280	285	
Phe Arg Asp Met Leu Leu			
290			

<210> 24
 <211> 300
 <212> PRT

<213> Caulobacter crescentus

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
1 5 10 15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
20 25 30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
35 40 45

Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
50 55 60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
65 70 75 80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
85 90 95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
100 105 110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile
115 120 125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140

Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
85 90 95

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
100 105 110

His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His
115 120 125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
130 135 140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys
145 150 155 160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
165 170 175

Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
180 185 190

Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
195 200 205

Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
210 215 220

Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
225 230 235 240

Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
245 250 255

Tyr Gln Glu Ile
260

<210> 26
<211> 289
<212> PRT
<213> Thermus thermophilus

<400> 26
Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
1 5 10 15
Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
20 25 30
Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
35 40 45
Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
50 55 60
Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
65 70 75 80
Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
85 90 95
Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu

100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
	165	170
		175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
	180	185
		190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly		
	195	200
		205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
	210	215
		220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
		240
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
	245	250
		255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
	260	265
		270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
	275	280
		285

Tyr

<210> 27

<211> 94

<212> DNA

<213> Thermus thermophilus

<400> 27

gccggaggga gaaaaaaaaa gccgagccca aggccccgcc cggccccacc ccgaagcgcc 60
 cgcacccccg ggccccccga ggaggaggag aggc 94

<210> 28
<211> 11
<212> PRT
<213> Thermus thermophilus

<400> 28
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (6)
<223> N at position 6 is either G or C

<220>
<221> unsure
<222> (12)
<223> N at position 12 is either G or C

<220>
<221> unsure
<222> (21)
<223> N at position 21 is either G or C

<400> 29
cacgcntacc tnttctccgg nac

23

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure

<222> (7)
<223> N at position 7 is either G or C

<220>
<221> unsure
<222> (10)
<223> N at position 10 is either G or C

<220>
<221> unsure
<222> (19)
<223> N at position 19 is either G or C

<220>
<221> unsure
<222> (22)
<223> N at position 22 is either G or C

<400> 30
gtgctcnggn ggctcctcnt cngtc 25

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tgggtcttgga tctcgatgaa gaa 33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggscststcs gagcagaag 29

<210> 33
<211> 34

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 33
 gcgggatacct caacgaggac ctctccatct tcaa 34

 <210> 34
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 34
 gcgggatacct tgtcgtcsag sgtsagsgcg tcgta 35

 <210> 35
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 35
 gggaaggacc agcgcgtact cccctgctc ctaggtgtg 39

 <210> 36
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 36
 gtgtggatcc ttcttcttsc ccatsgc 27

 <210> 37
 <211> 27

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 37
 caccgattcc agtggtgcct aggtgtg 27

 <210> 38
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 38
 caacacctgg tgttccagga gcctgtgctt 30

 <210> 39
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 39
 ccagaatcgt ctgctggtcg tag 23

 <210> 40
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 40
 agcaccctgg aggagcttc 19

 <210> 41
 <211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
catgtcgtac tgggtgtac

19

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (7)
<223> N at position 7 is A, C, G, or T

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (13)
<223> N at position 13 is A, C, G, or T

<220>
<221> unsure
<222> (14)
<223> N at position 14 is A, C, G, or T

<400> 42
gtsgtsnnsg acnnsagagac sacsggg

27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (9)

<223> N at position 9 is A, C, G, or T

<220>

<221> unsure

<222> (17)

<223> N at position 17 is A, C, G, or T

<220>

<221> unsure

<222> (18)

<223> N at position 18 is A, C, G, or T

<400> 43

gaasccsnng tcgaasnngg cgttgtg

27

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

cggggatcca cctcaatcac ctcgtgg

27

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

cggggatccg ccaccttgcg gctccgggtg

30

<210> 46
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 46
 gcgctctaga cgagttccca aagcgtgcgg t 31

 <210> 47
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 47
 cgcgctctaga tcacctgtat ccaga 25

 <210> 48
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 48
 gcggcgcata tgggtggtggt cctggacctg gag 33

 <210> 49
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 49
 cgcgctctaga tcacctgtat ccaga 25

<210> 50
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 50
 gtsctsgtsa agacscactt 20

 <210> 51
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 51
 sagsagsgcg ttgaasgtgt g 21

 <210> 52
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 52
 ctcgttggtg aaagtttccg tg 22

 <210> 53
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 53
 ctcgttggtg aaagtttccg tg 22

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 54
tctggcaaca cgttctggag cacatcc

27

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
tgctggcggt catcttcagg atg

23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
catcctgaag atgaacgcca gca

23

<210> 57
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
aggttatcca caggggtcat gtgca

25

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gtgtgtcata tgaacataac ggttcccaa 29

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
gcgcgaattc tcccttgtgg aaggcttag 29

<210> 60
<211> 13
<212> PRT
<213> Thermus thermophilus

<400> 60
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Thermus thermophilus

<400> 61
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
1 5 10

<210> 62
<211> 8

<212> PRT
<213> Thermus thermophilus

<400> 62
Phe Phe Ile Glu Ile Gln Asn His
1 5

<210> 63
<211> 8
<212> PRT
<213> Thermus thermophilus

<400> 63
Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

<210> 64
<211> 6
<212> PRT
<213> Thermus thermophilus

<400> 64
Ala Met Gly Lys Lys Lys
1 5

<210> 65
<211> 9
<212> PRT
<213> Thermus thermophilus

<400> 65
Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

<210> 66
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE

<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 66
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (4)
<223> Xaa at position 4 is undefined

<220>
<221> PEPTIDE
<222> (7)
<223> Xaa at position 7 is undefined

<400> 67
His Asn Ala Xaa Phe Asp Xaa Gly Phe
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 68
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 69
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 69
Val Leu Val Lys Thr His Leu
1 5

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 70
His Arg Ala Leu Tyr Asp
1 5

<210> 71
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 71
His Thr Phe Asn Ala Leu Leu
1 5

<210> 72
<211> 34
<212> PRT
<213> Escherichia coli

<400> 72
 Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
 1 5 10 15
 Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
 20 25 30
 Val Val

<210> 73
 <211> 34
 <212> PRT
 <213> *Vibrio cholerae*

<400> 73
 Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
 1 5 10 15
 Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
 20 25 30
 Val Val

<210> 74
 <211> 34
 <212> PRT
 <213> *Haemophilus influenzae*

<400> 74
 Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu
 1 5 10 15
 Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
 20 25 30
 Leu Val

<210> 75
 <211> 34
 <212> PRT
 <213> *Rickettsia prowazekii*

<400> 75

Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
1 5 10 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
20 25 30

Ile Val

<210> 76

<211> 34

<212> PRT

<213> *Helicobacter pylori*

<400> 76

Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
20 25 30

Ile Ile

<210> 77

<211> 34

<212> PRT

<213> *Synechocystis* sp.

<400> 77

Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
20 25 30

Ile Val

<210> 78

<211> 34

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 78

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> Escherichia coli

<400> 79

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80

<211> 46

<212> PRT

<213> Vibrio cholerae

<400> 80

Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81

<211> 46

<212> PRT

<213> Haemophilus influenzae

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 82

<211> 46

<212> PRT

<213> *Rickettsia prowazekii*

<400> 82

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
35 40 45

<210> 83

<211> 45

<212> PRT

<213> *Helicobacter pylori*

<400> 83

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
35 40 45

<210> 84

<211> 46

<212> PRT

<213> *Synechocystis* sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
35 40 45

<210> 85

<211> 46

<212> PRT

<213> Mycobacterium tuberculosis

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
1 5 10 15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

atgggcccggg agctccgctt cgcccacctc caccagcaca cccagttctc cctcctggac 60
ggggcggcga agctttccga cctcctcaag tgggtcaagg agacgacccc cgaggacccc 120
gccttgacca tgaccgacca cggcaacctc ttcggggccg tggagttcta caagaaggcc 180
accgaaatgg gcatcaagcc catcctgggc tacgaggcct acgtggcggc ggaaagccgc 240
tttgaccgca agcggggaaa gggcctagac gggggctact ttcacctcac cctcctcgcc 300
aaggacttca cgggggtacca gaacctggtg cgcttggcga gccgggctta cctggagggg 360
ttttacgaaa agccccgat tgaccgggag atcctgcgcg agcacgccga gggcctcatc 420
gccctctcgg ggtgcctcgg ggcggagatc cccagttca tcctccagga ccgtctggac 480
ctggccgagg cccggctcaa cgagtacctc tccatcttca aggaccgctt cttcatcgag 540
atccagaacc acggcctccc cgagcagaaa aaggtcaacg aggtcctcaa ggagttcgcc 600
cgaaagtacg gcctggggat ggtggccacc aacgacggcc attacgtgag gaaggaggac 660
gcccgcgccc acgaggtcct cctcgccatc cagtccaaga gcaccctgga cgaccccggg 720
cgctggcgct tcccctgcga cgagttctac gtgaagaccc ccgaggagat gcgggccatg 780
ttccccgagg aggagtgggg ggacgagccc tttgacaaca ccgtggagat cgcccgcacg 840

tgcaacgtgg	agctgcccac	cggggacaag	atgggtctacc	gaatcccccg	cttccccctc	900
cccagagggc	ggaccgaggc	ccagtacctc	atggagctca	ccttcaaggg	gctcctccgc	960
cgctaccccg	accggatcac	cgagggcttc	taccgggagg	tcttccgcct	tttggggaag	1020
cttccccccc	acggggacgg	ggaggccttg	gccgaggcct	tggcccaggt	ggagcgggag	1080
gcttgggaga	ggctcatgaa	gagcctcccc	cctttggccg	gggtcaagga	gtggacggcg	1140
gaggccatth	tccaccgggc	cctttacgag	ctttccgtga	tagagcgcat	ggggtttccc	1200
ggctacttcc	tcacgtcca	ggactacatc	aactgggccc	ggagaaacgg	cgtctccgtg	1260
ggggccggca	gggggagcgc	cgccgggagc	ctgggtggcct	acgccgtggg	gatcaccaac	1320
attgaccccc	tccgcttcgg	cctcctcttt	gagcgcttcc	tgaaccggga	gagggctctc	1380
atgcccagaca	ttgacacgga	cttctccgac	cgggagcggg	accgggtgat	ccagtacgtg	1440
cgggagcgct	acggcgagga	caaggtggcc	cagatcggca	ccctgggaag	cctcgcctcc	1500
aaggccgccc	tcaaggacgt	ggcccgggtc	tacggcatcc	cccacaagaa	ggcggaggaa	1560
ttggccaagc	tcaccccggt	gcagttcggg	aagcccaagc	ccctgcagga	ggccatccag	1620
gtggtgccgg	agcttagggc	ggagatggag	aaggacccca	aggtgcggga	ggctcctcag	1680
gtggccatgc	gcctggaggg	cctgaaccgc	cacgcctccg	tccacgccgc	cggggtggtg	1740
atcgccgccc	agcccctcac	ggacctcgtc	cccctcatgc	gcgaccagga	agggcggccc	1800
gtcaccacgt	acgacatggg	ggcgggtggag	gccttggggc	ttttgaagat	ggactttttg	1860
ggcctccgca	ccctcacctt	cctggacgag	gtcaagcgca	tcgtcaaggc	gtcccagggg	1920
gtggagctgg	actacgatgc	cctccccctg	gacgacccca	agaccttcgc	cctcctctcc	1980
cggggggaga	ccaagggggg	cttccagctg	gagtcggggg	ggatgaccgc	cacgctccgc	2040
ggcctcaagc	cgcggcgctt	tgaggacctg	atcgccatcc	tctccctcta	ccgccccggg	2100
cccatggagc	acatccccac	ctacatccgc	cgccaccacg	ggctggagcc	cgtgagctac	2160
agcgagtthc	cccacgccga	gaagtaccta	aagcccatcc	tggacgagac	ctacggcatc	2220
cccgtctacc	aggagcagat	catgcagatc	gcctcggccg	tggcggggta	ctccctgggc	2280
gaggcggacc	tcctgcggcg	gtccatgggc	aagaagaagg	tggaggagat	gaagtccac	2340
cgggagcgct	tcgtccaggg	ggccaaggaa	aggggcgtgc	ccgaggagga	ggccaaccgc	2400
ctctttgaca	tgctggaggc	cttcgccaac	tacggcttca	acaaatccca	cgtgcccgc	2460
tacagcctcc	tctcctacca	gaccgcctac	gtgaaggccc	actaccccgt	ggagtctcatg	2520
gccgcccctc	tctccgtgga	gcggcacgac	tccgacaagg	tggccgagta	catccgcgac	2580
gcccggggcca	tgggcataga	ggtccttccc	ccggacgtca	accgctccgg	gtttgacttc	2640
ctgggtccagg	gccggcagat	ccttttcggc	ctctccgcgg	tgaagaacgt	gggcgaggcg	2700
gcggcggagg	ccattctccg	ggagcgggag	cggggcggcc	cctaccggag	cctcggcgac	2760
ttcctcaagc	ggctggacga	gaaggtgctc	aacaagcgga	ccctggagtc	cctcatcaag	2820
gcgggcgccc	tggacggctt	cggggaaagg	gcgcggctcc	tcgcctccct	ggaagggtc	2880
ctcaagtggg	cggccgagaa	ccgggagaag	gcccgctcgg	gcattgatggg	cctcttcagc	2940
gaagtggagg	agccgcctth	ggccgaggcc	gccccctgg	acgagatcac	ccggtccgc	3000
tacgagaagg	aggccctggg	gatctacgtc	tccggccacc	ccatcttgcg	gtaccccggg	3060
ctccgggaga	cggccacctg	cacctggag	gagcttcccc	acctggcccg	ggacctgccg	3120
ccccgggtcta	gggtcctcct	tgccgggatg	gtggaggagg	tggtgcgcaa	gcccacaaag	3180
agcggcgggga	tgatggcccc	cttcgtcctc	tccgacgaga	cgggggcgct	tgaggcgggtg	3240
gcattcggcc	gggcctacga	ccaggtctcc	ccgaggctca	aggaggacac	ccccgtgctc	3300
gtcctcggcc	aggtggagcg	ggaggagggg	ggcgtgcggg	tgctggccca	ggccgttttg	3360
acctacgagg	agctggagca	ggtcccccg	gccctcgagg	tggagggtga	ggcctccctc	3420
ctggacgacc	gggggggtgg	ccacctgaaa	agcctcctgg	acgagcacgc	ggggaccctc	3480
cccctgtacg	tccgggtcca	gggcgccttc	ggcgaggccc	tcctcgccct	gagggagggtg	3540
cgggtggggg	aggaggctgt	aggcggccgc	gtggttccgg	gcctacctcc	tgcccgaccg	3600
ggaggtcctt	ctccagggcg	gccaggcggg	ggaggcccag	gaggcgggtg	ccttctaggg	3660
ggtgggcccgt	gagacctagc	gccatcgthc	tcgcccgggg	caaggaggcc	tgggcccgc	3720

cccttttgg

3729

<210> 87

<211> 1245

<212> PRT

<213> *Thermus thermophilus*

<400> 87

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
165 170 175

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
180 185 190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
195 200 205

Ala	Thr	Asn	Asp	Gly	His	Tyr	Val	Arg	Lys	Glu	Asp	Ala	Arg	Ala	His	210	215	220	
Glu	Val	Leu	Leu	Ala	Ile	Gln	Ser	Lys	Ser	Thr	Leu	Asp	Asp	Pro	Gly	225	230	235	240
Ala	Leu	Ala	Leu	Pro	Cys	Glu	Glu	Phe	Tyr	Val	Lys	Thr	Pro	Glu	Glu	245	250	255	
Met	Arg	Ala	Met	Phe	Pro	Glu	Glu	Glu	Val	Gly	Gly	Arg	Ser	Pro	Leu	260	265	270	
Thr	Thr	Pro	Trp	Arg	Ser	Pro	His	Val	Gln	Arg	Gly	Ala	Ala	Ile	Gly	275	280	285	
Thr	Arg	Trp	Ser	Thr	Arg	Ile	Pro	Arg	Phe	Pro	Leu	Pro	Glu	Gly	Arg	290	295	300	
Thr	Glu	Ala	Gln	Tyr	Leu	Met	Glu	Leu	Thr	Phe	Lys	Gly	Leu	Leu	Arg	305	310	315	320
Arg	Tyr	Pro	Asp	Arg	Ile	Thr	Glu	Gly	Phe	Tyr	Arg	Glu	Val	Phe	Arg	325	330	335	
Leu	Ser	Gly	Lys	Leu	Pro	Pro	His	Gly	Asp	Gly	Glu	Ala	Leu	Ala	Glu	340	345	350	
Ala	Leu	Ala	Gln	Val	Glu	Arg	Glu	Ala	Trp	Glu	Arg	Leu	Met	Lys	Ser	355	360	365	
Leu	Pro	Pro	Leu	Ala	Gly	Val	Lys	Glu	Trp	Thr	Ala	Glu	Ala	Ile	Phe	370	375	380	
His	Arg	Ala	Leu	Tyr	Glu	Leu	Ser	Ala	Ile	Glu	Arg	Met	Gly	Phe	Pro	385	390	395	400
Gly	Leu	Leu	Pro	His	Arg	Pro	Gly	Leu	His	Gln	Leu	Gly	Pro	Glu	Lys	405	410	415	
Gly	Val	Ser	Val	Gly	Pro	Gly	Arg	Gly	Gly	Ala	Ala	Gly	Ser	Leu	Val	420	425	430	
Ala	Tyr	Ala	Val	Gly	Ile	Thr	Asn	Ile	Asp	Pro	Leu	Arg	Phe	Gly	Leu	435	440	445	
Leu	Phe	Glu	Arg	Phe	Leu	Asn	Pro	Glu	Arg	Val	Ser	Met	Pro	Asp	Ile	450	455	460	

Asp	Thr	Asp	Phe	Ser	Asp	Arg	Glu	Arg	Asp	Arg	Val	Ile	Gln	Tyr	Val	465	470	475	480
Arg	Glu	Arg	Tyr	Gly	Glu	Asp	Lys	Val	Ala	Gln	Ile	Gly	Thr	Leu	Gly	485	490	495	
Ser	Leu	Ala	Ser	Lys	Ala	Ala	Leu	Lys	Glu	Val	Ala	Arg	Val	Tyr	Gly	500	505	510	
Ile	Pro	Arg	Lys	Lys	Ala	Glu	Glu	Leu	Ala	Lys	Leu	Ile	Pro	Val	Gln	515	520	525	
Phe	Gly	Lys	Pro	Lys	Pro	Leu	Gln	Glu	Ala	Ile	Gln	Val	Val	Pro	Glu	530	535	540	
Leu	Arg	Ala	Glu	Met	Glu	Lys	Asp	Pro	Lys	Val	Arg	Glu	Val	Leu	Glu	545	550	555	560
Val	Ala	Met	Arg	Leu	Glu	Gly	Leu	Asn	Arg	His	Ala	Ser	Val	His	Ala	565	570	575	
Gly	Arg	Gly	Gly	Val	Phe	Ser	Glu	Pro	Leu	Thr	Asp	Leu	Val	Pro	Leu	580	585	590	
Cys	Ala	Thr	Arg	Lys	Gly	Gly	Pro	Tyr	Thr	Gln	Tyr	Asp	Met	Gly	Ala	595	600	605	
Val	Glu	Ala	Leu	Gly	Leu	Leu	Lys	Met	Asp	Phe	Leu	Gly	Leu	Arg	Thr	610	615	620	
Leu	Thr	Phe	Leu	Asp	Glu	Val	Lys	Arg	Ile	Val	Lys	Ala	Ser	Gln	Gly	625	630	635	640
Val	Glu	Leu	Asp	Tyr	Asp	Ala	Leu	Pro	Leu	Asp	Asp	Pro	Lys	Thr	Phe	645	650	655	
Ala	Leu	Leu	Ser	Arg	Gly	Glu	Thr	Lys	Gly	Val	Phe	Gln	Leu	Glu	Ser	660	665	670	
Gly	Gly	Met	Thr	Ala	Thr	Leu	Arg	Gly	Leu	Lys	Pro	Arg	Arg	Phe	Glu	675	680	685	
Asp	Leu	Ile	Ala	Ile	Leu	Ser	Leu	Tyr	Arg	Pro	Gly	Pro	Met	Glu	His	690	695	700	
Ile	Pro	Thr	Tyr	Ile	Arg	Arg	His	His	Gly	Leu	Glu	Pro	Val	Ser	Tyr	705	710	715	720

Ser	Glu	Phe	Pro	His	Ala	Glu	Lys	Tyr	Leu	Lys	Pro	Ile	Leu	Asp	Glu	
				725					730					735		
Thr	Tyr	Gly	Ile	Pro	Val	Tyr	Gln	Glu	Gln	Ile	Met	Gln	Ile	Ala	Ser	
			740					745					750			
Ala	Val	Ala	Gly	Tyr	Ser	Leu	Gly	Glu	Ala	Asp	Leu	Leu	Arg	Arg	Ser	
		755					760					765				
Met	Gly	Lys	Lys	Lys	Val	Glu	Glu	Met	Lys	Ser	His	Arg	Glu	Arg	Phe	
	770					775					780					
Val	Gln	Gly	Ala	Lys	Glu	Arg	Gly	Val	Pro	Glu	Glu	Glu	Ala	Asn	Arg	
785					790					795					800	
Leu	Phe	Asp	Met	Leu	Glu	Ala	Phe	Ala	Asn	Tyr	Gly	Phe	Asn	Lys	Ser	
			805						810					815		
His	Ala	Ala	Ala	Tyr	Ser	Leu	Leu	Ser	Tyr	Gln	Thr	Ala	Tyr	Val	Lys	
			820					825					830			
Ala	His	Tyr	Pro	Val	Glu	Phe	Met	Ala	Ala	Leu	Leu	Ser	Val	Glu	Arg	
		835					840					845				
His	Asp	Ser	Asp	Lys	Val	Ala	Glu	Tyr	Ile	Arg	Asp	Ala	Arg	Ala	Met	
	850					855					860					
Gly	Ile	Glu	Val	Leu	Pro	Pro	Asp	Val	Asn	Arg	Ser	Gly	Phe	Asp	Phe	
865					870					875					880	
Leu	Val	Gln	Gly	Arg	Gln	Ile	Leu	Phe	Gly	Leu	Ser	Ala	Val	Lys	Asn	
			885						890					895		
Val	Gly	Glu	Ala	Ala	Ala	Glu	Ala	Ile	Leu	Arg	Glu	Arg	Glu	Arg	Gly	
			900					905					910			
Gly	Pro	Tyr	Arg	Ser	Leu	Gly	Asp	Phe	Leu	Lys	Arg	Leu	Asp	Glu	Lys	
		915					920					925				
Val	Leu	Asn	Lys	Arg	Thr	Leu	Glu	Ser	Leu	Ile	Lys	Ala	Gly	Ala	Leu	
	930					935					940					
Asp	Gly	Phe	Gly	Glu	Arg	Ala	Arg	Leu	Leu	Ala	Ser	Leu	Glu	Gly	Leu	
945					950					955					960	
Leu	Lys	Trp	Ala	Ala	Glu	Asn	Arg	Glu	Lys	Ala	Arg	Ser	Gly	Met	Met	
			965					970						975		

Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro
 980 985 990

Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile
 995 1000 1005

Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr
 1010 1015 1020

Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro
 1025 1030 1035 1040

Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg
 1045 1050 1055

Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp
 1060 1065 1070

Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln
 1075 1080 1085

Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu
 1090 1095 1100

Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp
 1105 1110 1115 1120

Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val
 1125 1130 1135

Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu
 1140 1145 1150

Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly
 1155 1160 1165

Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu
 1170 1175 1180

Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu
 1185 1190 1195 1200

Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg
 1205 1210 1215

Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala
 1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
1235 1240 1245

<210> 88
<211> 198
<212> PRT
<213> Thermus thermophilus

<400> 88

Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
1 5 10 15

Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
20 25 30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
35 40 45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg
50 55 60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
65 70 75 80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
85 90 95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
100 105 110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
115 120 125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
130 135 140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu
145 150 155 160

Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
165 170 175

Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
180 185 190

Tyr Met Leu Thr Ser Gly
195

<210> 89
 <211> 182
 <212> PRT
 <213> Deinococcus radiodurans

<220>
 <221> PEPTIDE
 <222> (79)
 <223> X at position 79 is undefined

<400> 89
 Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
 1 5 10 15
 Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
 20 25 30
 Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
 35 40 45
 Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
 50 55 60
 Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
 65 70 75 80
 Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
 85 90 95
 Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
 100 105 110
 Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
 115 120 125
 Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
 130 135 140
 Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
 145 150 155 160
 Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
 165 170 175
 Glu Leu Leu Gly Glu Arg
 180

<210> 90
 <211> 201
 <212> PRT
 <213> Bacillus subtilis

<400> 90
 His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
 1 5 10 15
 Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
 20 25 30
 Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
 35 40 45
 Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
 50 55 60
 Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
 65 70 75 80
 Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
 85 90 95
 Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
 100 105 110
 Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
 115 120 125
 Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
 130 135 140
 Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
 145 150 155 160
 His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 165 170 175
 His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
 180 185 190
 Lys Met Leu Lys Asp Ala Ala Glu Lys
 195 200

<210> 91
<211> 188
<212> PRT
<213> Haemophilus influenzae

<220>
<221> PEPTIDE
<222> (47)
<223> X at position 47 is undefined

<220>
<221> PEPTIDE
<222> (57)
<223> X at position 57 is undefined

<400> 91
Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
1 5 10 15
Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
20 25 30
Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
35 40 45
Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
50 55 60
His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
65 70 75 80
Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
85 90 95
His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
100 105 110
Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
115 120 125
Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
130 135 140
Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
145 150 155 160
Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
165 170 175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
180 185

<210> 92

<211> 189

<212> PRT

<213> Escherichia coli

<400> 92

Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
1 5 10 15

Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
20 25 30

Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
35 40 45

His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
50 55 60

His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
65 70 75 80

Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
85 90 95

His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu
100 105 110

Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
115 120 125

Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
130 135 140

Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu
145 150 155 160

His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
165 170 175

Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
180 185

<210> 93
 <211> 201
 <212> PRT
 <213> Helicobacter pylori

<400> 93
 Asn Leu Glu Tyr Leu Lys Ala Cys Gly Leu Asn Phe Ile Glu Thr Ser
 1 5 10 15
 Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu
 20 25 30
 Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys
 35 40 45
 His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile
 50 55 60
 Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr
 65 70 75 80
 Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro
 85 90 95
 Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser
 100 105 110
 Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg
 115 120 125
 Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys
 130 135 140
 Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu
 145 150 155 160
 Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg
 165 170 175
 Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu
 180 185 190
 Leu Asn Leu Pro Ser Tyr Ile Lys Thr
 195 200

<210> 94
 <211> 630

<212> DNA

<213> *Thermus thermophilus*

<400> 94

```
atggtggagc ggggtggtgcg gacccttctg gacgggaggt tcctcctgga ggaggggggtg 60
gggcttttggg agtggcgcta cccctttccc ctggaggggg aggcggtggt ggtcctggac 120
ctggagacca cggggccttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180
gaggggggga ggcgcctccc cttccagagc ctcgctccgc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcaccgg catcccccg gaggccctgg aggaggcccc ctccctggag 300
gaggttcttg agaaggccta ccccctccgc ggcgacgcca ccttggtgat ccacaacgcc 360
gcctttgacc tgggcttcc cgcgccggcc ttggagggcc tgggctaccg cctggaaaac 420
cccgtggtgg actccctgcg cttggccaga cggggcttac caggccttag gcgctacggc 480
ctggacgccc tctccgaggt cctggagctt ccccgaaagga cctgccaccg ggccctcgag 540
gacgtggagc gcaccctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttgggaact cgggaggtag                                     630
```

<210> 95

<211> 210

<212> PRT

<213> *Thermus thermophilus*

<400> 95

```
Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
  1              5              10              15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
      20              25              30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
      35              40              45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
      50              55              60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
      65              70              75              80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
      85              90              95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
      100             105             110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
      115             120             125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
```

130	135	140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly		
145	150	155 160
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His		
	165	170 175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val		
	180	185 190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly		
	195	200 205
Arg Glx		
210		
<210> 96		
<211> 461		
<212> PRT		
<213> Pseudomonas marcesans		
<400> 96		
Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn		
1	5	10 15
Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser		
	20	25 30
Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser		
	35	40 45
Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala		
	50	55 60
Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala		
	65	70 75 80
Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro		
	85	90 95
Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu		
	100	105 110
Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe		
	115	120 125

Asn	Arg	Phe	Val	Val	Gly	Pro	Asn	Ser	Arg	Met	Ala	His	Ala	Ala	Ala		
130						135					140						
Met	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe	Ile		
145					150					155					160		
Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	Gly		
				165					170					175			
His	Tyr	Arg	Leu	Glu	Ile	Asp	Pro	Gly	Ala	Lys	Val	Ser	Tyr	Val	Ser		
			180					185					190				
Thr	Glu	Thr	Phe	Thr	Asn	Asp	Leu	Ile	Leu	Ala	Ile	Arg	Gln	Asp	Arg		
		195					200					205					
Met	Gln	Ala	Phe	Arg	Asp	Arg	Tyr	Arg	Ala	Ala	Asp	Leu	Ile	Leu	Val		
	210					215					220						
Asp	Asp	Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	Phe		
225					230					235					240		
Phe	His	Thr	Phe	Asn	Ala	Leu	His	Asp	Ala	Gly	Ser	Gln	Ile	Val	Leu		
				245					250					255			
Ala	Ser	Asp	Arg	Pro	Pro	Ser	Gln	Ile	Pro	Arg	Leu	Gln	Glu	Arg	Leu		
			260					265					270				
Met	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Val	Gln	Ala	Pro	Asp		
		275					280					285					
Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	His	Glu	Arg		
	290					295					300						
Val	Gly	Leu	Pro	Arg	Asp	Leu	Ile	Gln	Phe	Ile	Ala	Gly	Arg	Phe	Thr		
305					310					315					320		
Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Thr	Arg	Ala	Ile	Ala	Phe		
				325					330					335			
Ala	Ser	Ile	Thr	Gly	Leu	Pro	Met	Thr	Val	Asp	Ser	Ile	Ala	Pro	Met		
			340					345					350				
Leu	Asp	Pro	Asn	Gly	Gln	Gly	Val	Glu	Val	Thr	Pro	Lys	Gln	Val	Leu		
		355					360					365					
Asp	Lys	Val	Ala	Glu	Val	Phe	Lys	Val	Thr	Pro	Asp	Glu	Met	Arg	Ser		
	370					375					380						

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
 385 390 395 400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr
 405 410 415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
 420 425 430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
 435 440 445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
 450 455 460

<210> 97

<211> 447

<212> PRT

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
 1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
 20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly
 35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
 50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
 65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
 85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
 100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
 115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
 130 135 140

Leu	Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile
145					150					155					160
Ala	His	Tyr	Arg	Leu	Glu	Met	Tyr	Pro	Asn	Ala	Lys	Val	Tyr	Tyr	Val
				165					170					175	
Ser	Thr	Glu	Arg	Phe	Thr	Asn	Asp	Leu	Ile	Thr	Ala	Ile	Arg	Gln	Asp
			180					185					190		
Asn	Met	Glu	Asp	Phe	Arg	Ser	Tyr	Tyr	Arg	Ser	Ala	Asp	Phe	Leu	Leu
		195					200					205			
Ile	Asp	Asp	Ile	Gln	Phe	Ile	Lys	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu
	210					215					220				
Phe	Phe	His	Thr	Phe	Asn	Ser	Leu	His	Glu	Ala	Gly	Lys	Gln	Val	Val
225					230					235					240
Val	Ala	Ser	Asp	Arg	Ala	Pro	Gln	Arg	Ile	Pro	Gly	Leu	Gln	Asp	Arg
				245					250					255	
Leu	Ile	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Ile	Gln	Val	Pro
			260					265					270		
Asp	Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	Tyr	Asp
		275					280					285			
Arg	Ile	Arg	Leu	Pro	Lys	Glu	Val	Ile	Glu	Tyr	Ile	Ala	Ser	His	Tyr
	290					295					300				
Thr	Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	Arg	Ala	Ile	Ala
305					310					315					320
Tyr	Thr	Ser	Leu	Ser	Asn	Val	Ala	Met	Thr	Val	Glu	Asn	Ile	Ala	Pro
				325					330					335	
Val	Leu	Asn	Pro	Pro	Val	Glu	Lys	Val	Ala	Ala	Ala	Pro	Glu	Thr	Ile
			340					345					350		
Ile	Thr	Ile	Val	Ala	Gln	His	Tyr	Gln	Leu	Lys	Val	Glu	Glu	Leu	Leu
		355					360					365			
Ser	Asn	Ser	Arg	Arg	Arg	Glu	Val	Ser	Leu	Ala	Arg	Gln	Val	Gly	Met
		370				375					380				
Tyr	Leu	Met	Arg	Gln	His	Thr	Asp	Leu	Ser	Leu	Pro	Arg	Ile	Gly	Glu
385					390					395					400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys

420	425	430
Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys		
435	440	445

<210> 99
 <211> 507
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 99
 Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
 1 5 10 15
 Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
 20 25 30
 Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu
 35 40 45
 Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
 50 55 60
 Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
 65 70 75 80
 Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
 85 90 95
 Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
 100 105 110
 Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
 115 120 125
 Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
 130 135 140
 His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
 145 150 155 160
 Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
 165 170 175
 Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala
 180 185 190

Ile Ala Glu Ala Pro Ala Arg Ala Tyr Asn Pro Leu Phe Ile Trp Gly
 195 200 205
 Glu Ser Gly Leu Gly Lys Thr His Leu Leu His Ala Ala Gly Asn Tyr
 210 215 220
 Ala Gln Arg Leu Phe Pro Gly Met Arg Val Lys Tyr Val Ser Thr Glu
 225 230 235 240
 Glu Phe Thr Asn Asp Phe Ile Asn Ser Leu Arg Asp Asp Arg Lys Val
 245 250 255
 Ala Phe Lys Arg Ser Tyr Arg Asp Val Asp Val Leu Leu Val Asp Asp
 260 265 270
 Ile Gln Phe Ile Glu Gly Lys Glu Gly Ile Gln Glu Glu Phe Phe His
 275 280 285
 Thr Phe Asn Thr Leu His Asn Ala Asn Lys Gln Ile Val Ile Ser Ser
 290 295 300
 Asp Arg Pro Pro Lys Gln Leu Ala Thr Leu Glu Asp Arg Leu Arg Thr
 305 310 315 320
 Arg Phe Glu Trp Gly Leu Ile Thr Asp Val Gln Pro Pro Glu Leu Glu
 325 330 335
 Thr Arg Ile Ala Ile Leu Arg Lys Lys Ala Gln Met Glu Arg Leu Ala
 340 345 350
 Val Pro Asp Asp Val Leu Glu Leu Ile Ala Ser Ser Ile Glu Arg Asn
 355 360 365
 Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Val Thr Ala Phe Ala Ser
 370 375 380
 Leu Asn Lys Thr Pro Ile Asp Lys Ala Leu Ala Glu Ile Val Leu Arg
 385 390 395 400
 Asp Leu Ile Ala Asp Ala Asn Thr Met Gln Ile Ser Ala Ala Thr Ile
 405 410 415
 Met Ala Ala Thr Ala Glu Tyr Phe Asp Thr Thr Val Glu Glu Leu Arg
 420 425 430
 Gly Pro Gly Lys Thr Arg Ala Leu Ala Gln Ser Arg Gln Ile Ala Met
 435 440 445

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
 450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile
 465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
 485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
 500 505

<210> 100
 <211> 446
 <212> PRT
 <213> Thermus thermophilus

<400> 100

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
 50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
 65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
 85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
 100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
 115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
 130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
 145 150 155 160

Phe	Pro	His	Met	Arg	Leu	Glu	Tyr	Val	Ser	Thr	Glu	Thr	Phe	Thr	Asn	
				165					170						175	
Glu	Leu	Ile	Asn	Arg	Pro	Ser	Ala	Arg	Asp	Arg	Met	Thr	Glu	Phe	Arg	
			180					185					190			
Glu	Arg	Tyr	Arg	Ser	Val	Asp	Leu	Leu	Leu	Val	Asp	Asp	Val	Gln	Phe	
		195					200					205				
Ile	Ala	Gly	Lys	Glu	Arg	Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn	
		210				215						220				
Ala	Leu	Tyr	Glu	Ala	His	Lys	Gln	Ile	Ile	Leu	Ser	Ser	Asp	Arg	Pro	
225					230					235					240	
Pro	Lys	Asp	Ile	Leu	Thr	Leu	Glu	Ala	Arg	Leu	Arg	Ser	Arg	Phe	Glu	
			245						250					255		
Trp	Gly	Leu	Ile	Thr	Asp	Asn	Pro	Ala	Pro	Asp	Leu	Glu	Thr	Arg	Ile	
		260						265					270			
Ala	Ile	Leu	Lys	Met	Asn	Ala	Ser	Ser	Gly	Pro	Glu	Asp	Pro	Glu	Asp	
		275					280					285				
Ala	Leu	Glu	Tyr	Ile	Ala	Arg	Gln	Val	Thr	Ser	Asn	Ile	Arg	Glu	Trp	
		290				295					300					
Glu	Gly	Ala	Leu	Met	Arg	Ala	Ser	Pro	Phe	Ala	Ser	Leu	Asn	Gly	Val	
305				310						315				320		
Glu	Leu	Thr	Arg	Ala	Val	Ala	Ala	Lys	Ala	Leu	Arg	His	Leu	Arg	Pro	
			325					330					335			
Arg	Glu	Leu	Glu	Ala	Asp	Pro	Leu	Glu	Ile	Ile	Arg	Lys	Ala	Ala	Gly	
		340						345					350			
Pro	Val	Arg	Pro	Glu	Thr	Pro	Gly	Gly	Ala	His	Gly	Glu	Arg	Arg	Lys	
		355					360					365				
Lys	Glu	Val	Val	Leu	Pro	Arg	Gln	Leu	Ala	Met	Tyr	Leu	Val	Arg	Glu	
		370				375					380					
Leu	Thr	Pro	Ala	Ser	Leu	Pro	Glu	Ile	Gly	Gln	Leu	Phe	Gly	Gly	Arg	
385					390					395					400	
Asp	His	Thr	Thr	Val	Arg	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Ala	
			405						410					415		

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
435 440 445

<210> 101

<211> 467

<212> PRT

<213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Ala Arg Gln Val Ala Asp Asn
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

180					185					190					
Lys	Pro	Asn	Ala	Lys	Val	Val	Tyr	Met	His	Ser	Glu	Arg	Phe	Val	Gln
		195					200					205			
Asp	Met	Val	Lys	Ala	Leu	Gln	Asn	Asn	Ala	Ile	Glu	Glu	Phe	Lys	Arg
	210					215					220				
Tyr	Tyr	Arg	Ser	Val	Asp	Ala	Leu	Leu	Ile	Asp	Asp	Ile	Gln	Phe	Phe
225					230					235					240
Ala	Asn	Lys	Glu	Arg	Ser	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn	Ala
				245					250					255	
Leu	Leu	Glu	Gly	Asn	Gln	Gln	Ile	Ile	Leu	Thr	Ser	Asp	Arg	Tyr	Pro
			260					265					270		
Lys	Glu	Ile	Asn	Gly	Val	Glu	Asp	Arg	Leu	Lys	Ser	Arg	Phe	Gly	Trp
		275					280					285			
Gly	Leu	Thr	Val	Ala	Ile	Glu	Pro	Pro	Glu	Leu	Glu	Thr	Arg	Val	Ala
	290					295					300				
Ile	Leu	Met	Lys	Lys	Ala	Asp	Glu	Asn	Asp	Ile	Arg	Leu	Pro	Gly	Glu
305					310					315					320
Val	Ala	Phe	Phe	Ile	Ala	Lys	Arg	Leu	Arg	Ser	Asn	Val	Arg	Glu	Leu
				325					330					335	
Glu	Gly	Ala	Leu	Asn	Arg	Val	Ile	Ala	Asn	Ala	Asn	Phe	Thr	Gly	Arg
			340					345					350		
Ala	Ile	Thr	Ile	Asp	Phe	Val	Arg	Glu	Ala	Leu	Arg	Asp	Leu	Leu	Ala
		355					360					365			
Leu	Gln	Glu	Lys	Leu	Val	Thr	Ile	Asp	Asn	Ile	Gln	Lys	Thr	Val	Ala
	370					375					380				
Glu	Tyr	Tyr	Lys	Ile	Lys	Val	Ala	Asp	Leu	Leu	Ser	Lys	Arg	Arg	Ser
385					390					395					400
Arg	Ser	Val	Ala	Arg	Pro	Arg	Gln	Met	Ala	Met	Ala	Leu	Ala	Lys	Glu
				405					410					415	
Leu	Thr	Asn	His	Ser	Leu	Pro	Glu	Ile	Gly	Asp	Ala	Phe	Gly	Gly	Arg
			420					425					430		
Asp	His	Thr	Thr	Val	Leu	His	Ala	Cys	Arg	Lys	Ile	Glu	Gln	Leu	Arg

435 440 445
 Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr
 450 455 460

 Leu Ser Ser
 465

 <210> 102
 <211> 440
 <212> PRT
 <213> *Thermatoga maritima*

 <400> 102
 Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys
 1 5 10 15

 Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly
 20 25 30

 Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu
 35 40 45

 Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu
 50 55 60

 Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His
 65 70 75 80

 Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr
 85 90 95

 Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly
 100 105 110

 Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly
 115 120 125

 Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr
 130 135 140

 His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp
 145 150 155 160

 Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val
 165 170 175

Asp Ser Met Lys Glu Gly Lys Leu Asn Glu Phe Arg Glu Lys Tyr Arg		
180	185	190
Lys Lys Val Asp Ile Leu Leu Ile Asp Asp Val Gln Phe Leu Ile Gly		
195	200	205
Lys Thr Gly Val Gln Thr Glu Leu Phe His Thr Phe Asn Glu Leu His		
210	215	220
Asp Ser Gly Lys Gln Ile Val Ile Cys Ser Asp Arg Glu Pro Gln Lys		
225	230	235 240
Leu Ser Glu Phe Gln Asp Arg Leu Val Ser Arg Phe Gln Met Gly Leu		
245	250	255
Val Ala Lys Leu Glu Pro Pro Asp Glu Glu Thr Arg Lys Ser Ile Ala		
260	265	270
Arg Lys Met Leu Glu Ile Glu His Gly Glu Leu Pro Glu Glu Val Leu		
275	280	285
Asn Phe Val Ala Glu Asn Val Asp Asp Asn Leu Arg Arg Leu Arg Gly		
290	295	300
Ala Ile Ile Lys Leu Leu Val Tyr Lys Glu Thr Thr Gly Lys Glu Val		
305	310	315 320
Asp Leu Lys Glu Ala Ile Leu Leu Leu Lys Asp Phe Ile Lys Pro Asn		
325	330	335
Arg Val Lys Ala Met Asp Pro Ile Asp Glu Leu Ile Glu Ile Val Ala		
340	345	350
Lys Val Thr Gly Val Pro Arg Glu Glu Ile Leu Ser Asn Ser Arg Asn		
355	360	365
Val Lys Ala Leu Thr Ala Arg Arg Ile Gly Met Tyr Val Ala Lys Asn		
370	375	380
Tyr Leu Lys Ser Ser Leu Arg Thr Ile Ala Glu Lys Phe Asn Arg Ser		
385	390	395 400
His Pro Val Val Val Asp Ser Val Lys Lys Val Lys Asp Ser Leu Leu		
405	410	415
Lys Gly Asn Lys Gln Leu Lys Ala Leu Ile Asp Glu Val Ile Gly Glu		
420	425	430

Ile Ser Arg Arg Ala Leu Ser Gly
 435 440

<210> 103

<211> 457

<212> PRT

<213> Helicobacter pylori

<400> 103

Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
 1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
 20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
 35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
 50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
 65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
 85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
 100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
 115 120 125

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
 130 135 140

Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
 145 150 155 160

Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
 165 170 175

Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
 180 185 190

Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
 195 200 205

<210> 104
 <211> 1305
 <212> DNA
 <213> Thermus thermophilus

<400> 104
 gtgtcgcacg aggccgtctg gcaacacggt ctggagcaca tccgccgcag catcaccgag 60
 gtggagttcc acacctgggt tgaaaggatc cgccccttgg ggatccggga cggggtgctg 120
 gagctcgccg tgcccacctc ctttgccctg gactggatcc ggcgccacta cgccggcctc 180
 atccaggagg gccctcgggt cctcggggcc caggcgcccc ggtttgagct ccgggtggtg 240
 cccgggggtc tagtccagga ggacatcttc cagcccccg cagagcccccc ggcccaagct 300
 caacccgaag atacctttaa aacttcgtgg tggggcccaa caactccatg gcccacggc 360
 ggcgccgtgg ccgtggccga gtcccccggc cgggcctaca accccctctt catctacggg 420
 ggccgtggcc tgggaaagac ctacctgatg cagccgtgg gccactccg tgcgaagcgc 480
 ttccccaca tgagattaga gtacgtttcc acggaactt tcaccaacga gctcatcaac 540
 cggccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtggacctc 600
 ctgctggtgg acgacgtcca gtteatcgcc ggaaaggagc gcaccagga ggagtttttc 660
 cacaccttca acgcccttta cgaggccac aagcagatca tcctctctc cgaccggccg 720
 cccaaggaca tcctcacctt ggaggcgcgc ctgcggagcc gctttgagtg gggcctgatc 780
 accgacaatc cagccccga cctggaaacc cggatcgcca tcctgaagat gaacgccagc 840
 agcgggcctg aggatcccga ggacgccctg gagtacatcg ccggcaggt cacctccaac 900
 atccgggagt ggggaagggc cctcatgcgg gcatcgctt tcgcctccct caacggcggt 960
 gagctgacct gcgccgtggc ggccaaggct ctccgacatc ttgcgccag ggagctggag 1020
 gcggacctt tggagatcat ccgcaaagcg gcgggaccag ttcggcctga aaccccgga 1080
 ggagctcacg gggagcgccg caagaaggag gtggctctcc ccggcagct cgccatgtac 1140
 ctggtgcggg agctacccc ggctccctg cccgagatcg accagctcaa cgacgaccgg 1200
 gaccacacca cggctctcta cgccatccag aaggtccagg agctcgcgga aagcgaccgg 1260
 gaggtgcagg gcctcctccg caccctccgg gaggcgtgca catga 1305

<210> 105
 <211> 434
 <212> PRT
 <213> Thermus thermophilus

<400> 105
 Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15
 Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30
 Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45
 Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly

50		55		60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val				
65		70		80
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro				
	85		90	95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly				
	100		105	110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser				
	115		120	125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu				
	130		135	140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg				
145		150		160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn				
	165		170	175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg				
	180		185	190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe				
	195		200	205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn				
	210		215	220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro				
225		230		240
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu				
	245		250	255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile				
	260		265	270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp				
	275		280	285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp				
	290		295	300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val				

305		310		315		320
Glu Leu Thr Arg	Ala Val Ala Ala Lys	Ala Leu Arg His	Leu Arg Pro			
	325		330		335	
Arg Glu Leu Glu	Ala Asp Pro Leu	Glu Ile Ile Arg	Lys Ala Ala Gly			
	340		345		350	
Pro Val Arg Pro	Glu Thr Pro Gly	Gly Ala His Gly	Glu Arg Arg Lys			
	355		360		365	
Lys Glu Val Val	Leu Pro Arg Gln	Leu Ala Met Tyr	Leu Val Arg Glu			
	370		375		380	
Leu Thr Pro Ala	Ser Leu Pro Glu	Ile Asp Gln Leu	Asn Asp Asp Arg			
385		390		395		400
Asp His Thr Thr	Val Leu Tyr Ala	Ile Gln Lys Val	Gln Glu Leu Ala			
	405		410		415	
Glu Ser Asp Arg	Glu Val Gln Gly	Leu Leu Arg Thr	Leu Arg Glu Ala			
	420		425		430	

Cys Thr

<210> 106
 <211> 1128
 <212> DNA
 <213> Thermus thermophilus

<400> 106

atgaacataa	cggttcccaa	aaaactcctc	toggaccagc	tttccctcct	ggagcgcac	60
gtcccctcta	gaagcgccaa	ccccctctac	acctacctgg	ggctttacgc	cgaggaaggg	120
gccttgatcc	tcttcgggac	caacggggag	gtggacctcg	aggtccgcct	ccccgccgag	180
gccccaaagcc	ttccccgggt	gctcgtcccc	gccagaccct	tcttccagct	ggtgcggagc	240
cttctgggg	acctcgtggc	cctcggcctc	gcctcggagc	cgggccaggg	ggggcagctg	300
gagctctcct	cggggcgttt	ccgcacccgg	ctcagcctgg	ccctgccga	gggctacccc	360
gagcttctgg	tgcccgaggg	ggaggacaag	ggggccttcc	ccctccggac	gcggatgccc	420
tccggggagc	tcgtcaaggc	cttgacccac	gtgcgctacg	ccgcgagcaa	cgaggagtac	480
cgggccatct	tccgcggggg	gcagctggag	ttctcccccc	agggcttccg	ggcgggtggcc	540
tccgacgggt	accgcctcgc	cctctacgac	ctgcccctgc	cccaagggtt	ccaggccaag	600
gccgtggtcc	ccgcccggag	cgtggacgag	atgggtgcggg	tcctgaaggg	ggcggacggg	660
gccgaggccg	tcctcgccct	gggcgagggg	gtgttgggcc	tggccctcga	gggcggaagc	720
gggggtccgga	tggccctccg	cctcatggaa	ggggagttcc	ccgactacca	gagggtcac	780
ccccaggagt	tcgccctcaa	ggtccaggtg	gagggggagg	ccctcagggg	ggcgggtgcgc	840
cgggtgagcg	tcctctccga	ccggcagaa	caccgggtgg	acctcctttt	ggaggaaggc	900

cggatcctcc tctccgccga gggggactac ggcaaggggc aggaggaggt gcccgccag 960
 gtggaggggc cggacatggc cgtggcctac aacgcccgt acctcctcga ggccctcgcc 1020
 cccgtggggg accgggcca cctgggcata tccgggcca cgagcccgag cctcatctgg 1080
 ggggacgggg aggggtaccg ggcggtggtg gtgccctca ggtctag 1128

<210> 107

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 107

Met	Asn	Ile	Thr	Val	Pro	Lys	Lys	Leu	Leu	Ser	Asp	Gln	Leu	Ser	Leu
1				5				10					15		

Leu	Glu	Arg	Ile	Val	Pro	Ser	Arg	Ser	Ala	Asn	Pro	Leu	Tyr	Thr	Tyr
			20					25					30		

Leu	Gly	Leu	Tyr	Ala	Glu	Glu	Gly	Ala	Leu	Ile	Leu	Phe	Gly	Thr	Asn
		35					40					45			

Gly	Glu	Val	Asp	Leu	Glu	Val	Arg	Leu	Pro	Ala	Glu	Ala	Gln	Ser	Leu
	50					55					60				

Pro	Arg	Val	Leu	Val	Pro	Ala	Gln	Pro	Phe	Phe	Gln	Leu	Val	Arg	Ser
65					70				75					80	

Leu	Pro	Gly	Asp	Leu	Val	Ala	Leu	Gly	Leu	Ala	Ser	Glu	Pro	Gly	Gln
			85					90						95	

Gly	Gly	Gln	Leu	Glu	Leu	Ser	Ser	Gly	Arg	Phe	Arg	Thr	Arg	Leu	Ser
		100						105					110		

Leu	Ala	Pro	Ala	Glu	Gly	Tyr	Pro	Glu	Leu	Leu	Val	Pro	Glu	Gly	Glu
		115				120						125			

Asp	Lys	Gly	Ala	Phe	Pro	Leu	Arg	Thr	Arg	Met	Pro	Ser	Gly	Glu	Leu
	130					135					140				

Val	Lys	Ala	Leu	Thr	His	Val	Arg	Tyr	Ala	Ala	Ser	Asn	Glu	Glu	Tyr
145					150					155					160

Arg	Ala	Ile	Phe	Arg	Gly	Val	Gln	Leu	Glu	Phe	Ser	Pro	Gln	Gly	Phe
			165					170						175	

Arg	Ala	Val	Ala	Ser	Asp	Gly	Tyr	Arg	Leu	Ala	Leu	Tyr	Asp	Leu	Pro
			180					185					190		

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205
 Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220
 Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240
 Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255
 Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270
 Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285
 Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300
 Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320
 Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335
 Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350
 Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365
 Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 108

<211> 376

<212> PRT

<213> Thermus thermophilus

<400> 108

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
 1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
 20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35 40 45
 Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50 55 60
 Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65 70 75 80
 Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85 90 95
 Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
 100 105 110
 Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
 115 120 125
 Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
 130 135 140
 Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
 145 150 155 160
 Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
 165 170 175
 Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
 180 185 190
 Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205
 Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220
 Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240
 Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255
 Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270
 Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
 50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
 65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
 85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115		120		125											
Thr	Leu	Pro	Gln	Ala	Thr	Met	Lys	Arg	Leu	Ile	Glu	Ala	Thr	Gln	Phe
130						135					140				
Ser	Met	Ala	His	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Phe
145					150					155					160
Glu	Thr	Glu	Gly	Glu	Glu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg
				165					170					175	
Leu	Ala	Val	Cys	Ser	Met	Pro	Ile	Gly	Gln	Ser	Leu	Pro	Ser	His	Ser
			180					185					190		
Val	Ile	Val	Pro	Arg	Lys	Gly	Val	Ile	Glu	Leu	Met	Arg	Met	Leu	Asp
	195						200					205			
Gly	Gly	Asp	Asn	Pro	Leu	Arg	Val	Gln	Ile	Gly	Ser	Asn	Asn	Ile	Arg
210						215					220				
Ala	His	Val	Gly	Asp	Phe	Ile	Phe	Thr	Ser	Lys	Leu	Val	Asp	Gly	Arg
225					230					235					240
Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Lys	Asn	Pro	Asp	Lys	His	Leu
				245					250					255	
Glu	Ala	Gly	Cys	Asp	Leu	Leu	Lys	Gln	Ala	Phe	Ala	Arg	Ala	Ala	Ile
			260					265					270		
Leu	Ser	Asn	Glu	Lys	Phe	Arg	Gly	Val	Arg	Leu	Tyr	Val	Ser	Glu	Asn
	275						280					285			
Gln	Leu	Lys	Ile	Thr	Ala	Asn	Asn	Pro	Glu	Gln	Glu	Glu	Ala	Glu	Glu
290						295					300				
Ile	Leu	Asp	Val	Thr	Tyr	Ser	Gly	Ala	Glu	Met	Glu	Ile	Gly	Phe	Asn
305					310				315						320
Val	Ser	Tyr	Val	Leu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Cys	Glu	Asn	Val
			325					330					335		
Arg	Met	Met	Leu	Thr	Asp	Ser	Val	Ser	Ser	Val	Gln	Ile	Glu	Asp	Ala
			340					345					350		
Ala	Ser	Gln	Ser	Ala	Ala	Tyr	Val	Val	Met	Pro	Met	Arg	Leu	Glx	
	355						360					365			

<210> 110
 <211> 367
 <212> PRT
 <213> Proteus mirabilis

<400> 110

Met	Lys	Phe	Ile	Ile	Glu	Arg	Glu	Gln	Leu	Leu	Lys	Pro	Leu	Gln	Gln	1	5	10	15
Val	Ser	Gly	Pro	Leu	Gly	Gly	Arg	Pro	Thr	Leu	Pro	Ile	Leu	Gly	Asn	20	25	30	
Leu	Leu	Leu	Lys	Val	Thr	Glu	Asn	Thr	Leu	Ser	Leu	Thr	Gly	Thr	Asp	35	40	45	
Leu	Glu	Met	Glu	Met	Met	Ala	Arg	Val	Ser	Leu	Ser	Gln	Ser	His	Glu	50	55	60	
Ile	Gly	Ala	Thr	Thr	Val	Pro	Ala	Arg	Lys	Phe	Phe	Asp	Ile	Trp	Arg	65	70	75	80
Gly	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Ser	Val	Glu	Leu	Asp	Gly	Asp	Arg	85	90	95	
Leu	Leu	Val	Arg	Ser	Gly	Arg	Ser	Arg	Phe	Ser	Leu	Ser	Thr	Leu	Pro	100	105	110	
Ala	Ser	Asp	Phe	Pro	Asn	Leu	Asp	Asp	Trp	Gln	Ser	Glu	Val	Glu	Phe	115	120	125	
Thr	Leu	Pro	Gln	Ala	Thr	Leu	Lys	Arg	Leu	Ile	Glu	Ser	Thr	Gln	Phe	130	135	140	
Ser	Met	Ala	His	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Phe	145	150	155	160
Glu	Thr	Glu	Asn	Thr	Glu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg	165	170	175	
Leu	Ala	Val	Cys	Ala	Met	Asp	Ile	Gly	Gln	Ser	Leu	Pro	Gly	His	Ser	180	185	190	
Val	Ile	Val	Pro	Arg	Lys	Gly	Val	Ile	Glu	Leu	Met	Arg	Leu	Leu	Asp	195	200	205	
Gly	Ser	Gly	Glu	Ser	Leu	Leu	Gln	Leu	Gln	Ile	Gly	Ser	Asn	Asn	Leu	210	215	220	

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
 225 230 235 240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
 245 250 255

Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
 260 265 270

Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
 275 280 285

Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
 290 295 300

Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
 305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
 325 330 335

Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
 340 345 350

Val Ala Ser Ala Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
 355 360 365

<210> 111

<211> 366

<212> PRT

<213> Haemophilus influenzae

<400> 111

Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15

Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
 20 25 30

Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Ser Glu
 50 55 60

Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg
 65 70 75 80

Thr Leu Ser Asp Asp Ser Glu Ile Thr Val Thr Phe Glu Gln Asp Arg
 85 90 95
 Ala Leu Val Gln Ser Gly Arg Ser Arg Phe Thr Leu Ala Thr Gln Pro
 100 105 110
 Ala Glu Glu Tyr Pro Asn Leu Thr Asp Trp Gln Ser Glu Val Asp Phe
 115 120 125
 Glu Leu Pro Gln Asn Thr Leu Arg Arg Leu Ile Glu Ala Thr Gln Phe
 130 135 140
 Ser Met Ala Asn Gln Asp Ala Arg Tyr Phe Leu Asn Gly Met Lys Phe
 145 150 155 160
 Glu Thr Glu Gly Asn Leu Leu Arg Thr Val Ala Thr Asp Gly His Arg
 165 170 175
 Leu Ala Val Cys Thr Ile Ser Leu Glu Gln Glu Leu Gln Asn His Ser
 180 185 190
 Val Ile Leu Pro Arg Lys Gly Val Leu Glu Leu Val Arg Leu Leu Glu
 195 200 205
 Thr Asn Asp Glu Pro Ala Arg Leu Gln Ile Gly Thr Asn Asn Leu Arg
 210 215 220
 Val His Leu Lys Asn Thr Val Phe Thr Ser Lys Leu Ile Asp Gly Arg
 225 230 235 240
 Phe Pro Asp Tyr Arg Arg Val Leu Pro Arg Asn Ala Thr Lys Ile Val
 245 250 255
 Glu Gly Asn Trp Glu Met Leu Lys Gln Ala Phe Ala Arg Ala Ser Ile
 260 265 270
 Leu Ser Asn Glu Arg Ala Arg Ser Val Arg Leu Ser Leu Lys Glu Asn
 275 280 285
 Gln Leu Lys Ile Thr Ala Ser Asn Thr Glu His Glu Glu Ala Glu Glu
 290 295 300
 Ile Val Asp Val Asn Tyr Asn Gly Glu Glu Leu Glu Val Gly Phe Asn
 305 310 315 320
 Val Thr Tyr Ile Leu Asp Val Leu Asn Ala Leu Lys Cys Asn Gln Val
 325 330 335

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
 340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
 355 360 365

<210> 112

<211> 367

<212> PRT

<213> Pseudomonas putida

<400> 112

Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
 1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
 20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
 50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
 65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
 85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
 100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
 115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
 130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
 165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His

180	185	190
Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu		
195	200	205
Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile		
210	215	220
Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly		
225	230	235 240
Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu		
245	250	255
Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala		
260	265	270
Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala		
275	280	285
Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu		
290	295	300
Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe		
305	310	315 320
Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln		
325	330	335
Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu		
340	345	350
Ala Gly Asn Asp Asp Ser Ser Tyr Val Val Met Pro Met Arg Leu		
355	360	365

<210> 113
 <211> 366
 <212> PRT
 <213> Buchnera aphidicola

<400> 113
 Met Lys Phe Thr Ile Gln Asn Asp Ile Leu Thr Lys Asn Leu Lys Lys
 1 5 10 15
 Ile Thr Arg Val Leu Val Lys Asn Ile Ser Phe Pro Ile Leu Glu Asn
 20 25 30

Ile Leu Ile Gln Val Glu Asp Gly Thr Leu Ser Leu Thr Thr Thr Asn
 35 40 45
 Leu Glu Ile Glu Leu Ile Ser Lys Ile Glu Ile Ile Thr Lys Tyr Ile
 50 55 60
 Pro Gly Lys Thr Thr Ile Ser Gly Arg Lys Ile Leu Asn Ile Cys Arg
 65 70 75 80
 Thr Leu Ser Glu Lys Ser Lys Ile Lys Met Gln Leu Lys Asn Lys Lys
 85 90 95
 Met Tyr Ile Ser Ser Glu Asn Ser Asn Tyr Ile Leu Ser Thr Leu Ser
 100 105 110
 Ala Asp Thr Phe Pro Asn His Gln Asn Phe Asp Tyr Ile Ser Lys Phe
 115 120 125
 Asp Ile Ser Ser Asn Ile Leu Lys Glu Met Ile Glu Lys Thr Glu Phe
 130 135 140
 Ser Met Gly Lys Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160
 Glu Lys Lys Asp Lys Phe Leu Arg Ser Val Ala Thr Asp Gly Tyr Arg
 165 170 175
 Leu Ala Ile Ser Tyr Thr Gln Leu Lys Lys Asp Ile Asn Phe Phe Ser
 180 185 190
 Ile Ile Ile Pro Asn Lys Ala Val Met Glu Leu Leu Lys Leu Leu Asn
 195 200 205
 Thr Gln Pro Gln Leu Leu Asn Ile Leu Ile Gly Ser Asn Ser Ile Arg
 210 215 220
 Ile Tyr Thr Lys Asn Leu Ile Phe Thr Thr Gln Leu Ile Glu Gly Glu
 225 230 235 240
 Tyr Pro Asp Tyr Lys Ser Val Leu Phe Lys Glu Lys Lys Asn Pro Ile
 245 250 255
 Ile Thr Asn Ser Ile Leu Leu Lys Lys Ser Leu Leu Arg Val Ala Ile
 260 265 270
 Leu Ala His Glu Lys Phe Cys Gly Ile Glu Ile Lys Ile Glu Asn Gly
 275 280 285

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
 290 295 300
 Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
 305 310 315 320
 Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
 325 330 335
 Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu
 340 345 350
 Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
 355 360 365

<210> 114
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 114
 gtgtggatcc tcgtccccct catgcgcgac caggaaggg 39

<210> 115
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 115
 gtgtggatcc gtggtgacct tagccac 27

<210> 116
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 116

ttcgtgtccg aggaccttgt ggtccacaac

30

<210> 117

<211> 3514

<212> DNA

<213> *Aquifex aeolicus*

<400> 117

```
atgagtaagg atttcgtcca ccttcacctg cacacccagt tctcactcct ggacggggct 60
ataaagatag acgagctcgt gaaaaaggca aaggagtatg gatacaaagc tgtcggaatg 120
tcagaccacg gaaacctctt cggttcgtat aaattctaca aagccctgaa ggcggaagga 180
attaagccca taatcggcat ggaagcctac tttaccacgg gttcgagggt tgacagaaag 240
actaaaacga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatagca 300
aaggacgaaa aggtctaaag aacttaatga agctctcaac cctcgcctac aaagaagggt 360
tttactacaa acccagaatt gattacgaac tccttgaaaa gtacggggag ggcctaatag 420
cccttaccgc atgcctgaaa ggtgttccca cctactacgc ttctataaac gaagtgaaaa 480
aggcggagga atgggtaaag aagttcaagg atatatcgg agatgacctt tatttagaac 540
ttcaagcgaa caacattcca gaacaggaag tggcaaacag gaacttaata gagatagcca 600
aaaagtacga tgtgaaactc atagcgacgc aggacgcca ctacctcaat cccgaagaca 660
ggtacgcca cacggttctt atggcacttc aaatgaaaaa gaccattcac gaactgagtt 720
cgggaaactt caagtgttca aacgaagacc ttcactttgc tccacccgag tacatgtgga 780
aaaagtttga aggttaagttc gaaggctggg aaaaggcact cctgaacact ctcgaggtaa 840
tggaagagac agcggacagc tttgagatat ttgaaaactc cacctacctc cttcccaagt 900
acgacgttcc gcccgacaaa acccttgagg aatacctcag agaactcgcg taaaagggtt 960
taagacagag gatagaaagg ggacaagcta aggatactaa agagtactgg gagaggctcg 1020
agtacgaact ggaagttata aacaaaatgg gctttgctgg atacttcttg atagttcagg 1080
acttcataaa ctgggctaag aaaaacgaca tacctgttgg acccggaagg ggaagtgctg 1140
gaggttcctt cgtcgcatac gccatcggaa taacggacgt tgacctata aagcacggat 1200
tcctttttga gaggttctta aaccccgaaa gggtttccat gccggatata gacgtggatt 1260
tctgtcagga caacaggga aaggtcatag agtacgtaag gaacaagtac ggacacgaca 1320
acgtagctca gataatcacc tacaacgtaa tgaaggcgaa gcaaacactg agagacgtcg 1380
caagggccat gggactcccc tactccaccg cggacaaact cgcaaaactc attcctcagg 1440
gggacgttca gggaacgtgg ctcagtctgg aagagatgta caaaacgcct gtggaggaac 1500
tccttcagaa gtacggagaa cacagaacgg acatagagga caacgtaaag aagttcagac 1560
agatatgcga agaaagtccg gagataaaac agctcgttga gacggccctg aagcttgaag 1620
gtctcacgag acacacctcc ctccacgccg cgggagtggg tatagacca aagcccttga 1680
gcgagctcgt tcccctctac tacgataaag agggcgaggt cgcaaccag tacgacatgg 1740
ttcagctcga agaactcggg ctctgaaga tggacttctt cggactcaaa accctcacag 1800
aactgaaact catgaaagaa ctcataaagg aaagacacgg agtggatata aacttccttg 1860
aacttcccct tgacgacctg aaagtattaca aactccttca ggaaggaaaa accacgggag 1920
tgttccagct cgaaagcagg ggaatgaaag aactcctgaa gaaactaaag cccgacagct 1980
ttgacgacat cgttgcggtc ctgcgactct acagaccggg acctctaaag agcggactcg 2040
ttgacacata cattaagaga aagcacggaa aagaaccggt tgagtacccc ttcccggagc 2100
ttgaaccggt ccttaaggaa acctacggag taatcgttta tcaggaacag gtgatgaaga 2160
tgtctcagat actttccggc tttactcccg gagaggcgga taccctcaga aaggcgatag 2220
gtaagaagaa agcggattta atggctcaga tgaaagacaa gttcatacag ggagcgggtg 2280
```

```

aaaggggata ccctgaagaa aagataagga agctctggga agacatagag aagttcgctt 2340
cctactcctt caacaagtct cactcggttag cttacgggta catctcctac tggaccgcct 2400
acgttaaagc ccactatccc gcggagttct tcgcggtaaa actcacaact gaaaagaacg 2460
acaacaagtt cctcaacctc ataaaagacg ctaaactctt cggatttgag atacttcccc 2520
ccgacataaa caagagtgat gtaggattta cgatagaagg tgaaaacagg ataaggttcg 2580
ggcttgcgag gataaaggga gtgggagagg aaactgctaa gataatcggt gaagctagaa 2640
agaagtataa gcagttcaaa gggcttgcgg acttcataaa caaaaccaag aacaggaaga 2700
taaacaagaa agtcgtggaa gcactcgtaa aggcaggggc ttttgacttt actaagaaaa 2760
agaggaaaga actactcgct aaagtggcaa actctgaaaa agcattaatg gctacacaaa 2820
actccctttt cgggtgcaccg aaagaagaag tggaagaact cgaccctta aagcttgaaa 2880
aggaagttct cggtttttac atttcagggc accccttga caactacgaa aagctcctca 2940
agaaccgcta cacaccatt gaagatttag aagagtggga caaggaaagc gaagcgggtgc 3000
ttacaggagt tatcacggaa ctcaaagtaa aaaagacgaa aaacggagat tacatggcgg 3060
tcttcaacct cgttgacaag acgggactaa tagagtgtgt cgtcttcccg ggagtttacg 3120
aagaggcaaa ggaactgata gaagaggaca gagtagtggt agtcaaagggt tttctggacg 3180
aggaccttga aacggaaaat gtcaagttcg tggtgaaaga ggttttctcc cctgaggagt 3240
tcgcaaagga gatgaggaat accctttata tattcttaaa aagagagcaa gccctaaacg 3300
gcgttgccga aaaactaaag ggaattattg aaaacaacag gacggaggac ggatacaact 3360
tggttctcac ggttgatctg ggagactact tcgttgattt agcactocca caagatatga 3420
aactaaaggc tgacagaaag gttgtagagg agatagaaaa actgggagtg aaggtcataa 3480
tttagtaaat aacccttact tccgagtagt cccc 3514

```

<210> 118

<211> 1161

<212> PRT

<213> Aquifex aeolicus

<400> 118

```

Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu
  1                      5                      10                      15

```

```

Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
          20                      25                      30

```

```

Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
      35                      40                      45

```

```

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
      50                      55                      60

```

```

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
      65                      70                      75                      80

```

```

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
          85                      90                      95

```

```

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu

```

100	105	110
Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp		
115	120	125
Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala		
130	135	140
Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys		
145	150	155
Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp		
	165	170
Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala		
	180	185
Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile		
	195	200
Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His		
	210	215
Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser		
225	230	235
Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro		
	245	250
Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys		
	260	265
Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe		
	275	280
Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro		
	290	295
Pro Asp Lys Thr Leu Glu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly		
305	310	315
Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr		
	325	330
Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe		
	340	345
Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys		

355		360		365	
Asn Asp Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Gly Gly Ser Leu					
370		375		380	
Val Ala Tyr Ala Ile Gly Ile Thr Asp Val Asp Pro Ile Lys His Gly					
385		390		395	400
Phe Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp					
	405		410		415
Ile Asp Val Asp Phe Cys Gln Asp Asn Arg Glu Lys Val Ile Glu Tyr					
	420		425		430
Val Arg Asn Lys Tyr Gly His Asp Asn Val Ala Gln Ile Ile Thr Tyr					
	435		440		445
Asn Val Met Lys Ala Lys Gln Thr Leu Arg Asp Val Ala Arg Ala Met					
	450		455		460
Gly Leu Pro Tyr Ser Thr Ala Asp Lys Leu Ala Lys Leu Ile Pro Gln					
465		470		475	480
Gly Asp Val Gln Gly Thr Trp Leu Ser Leu Glu Glu Met Tyr Lys Thr					
	485		490		495
Pro Val Glu Glu Leu Leu Gln Lys Tyr Gly Glu His Arg Thr Asp Ile					
	500		505		510
Glu Asp Asn Val Lys Lys Phe Arg Gln Ile Cys Glu Glu Ser Pro Glu					
	515		520		525
Ile Lys Gln Leu Val Glu Thr Ala Leu Lys Leu Glu Gly Leu Thr Arg					
	530		535		540
His Thr Ser Leu His Ala Ala Gly Val Val Ile Ala Pro Lys Pro Leu					
545		550		555	560
Ser Glu Leu Val Pro Leu Tyr Tyr Asp Lys Glu Gly Glu Val Ala Thr					
	565		570		575
Gln Tyr Asp Met Val Gln Leu Glu Glu Leu Gly Leu Leu Lys Met Asp					
	580		585		590
Phe Leu Gly Leu Lys Thr Leu Thr Glu Leu Lys Leu Met Lys Glu Leu					
	595		600		605
Ile Lys Glu Arg His Gly Val Asp Ile Asn Phe Leu Glu Leu Pro Leu					

610	615	620
Asp Asp Pro Lys Val Tyr Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly		
625	630	635 640
Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu		
	645	650 655
Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg		
	660	665 670
Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys		
	675	680 685
His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val		
	690	695 700
Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys		
705	710	715 720
Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu		
	725	730 735
Arg Lys Ala Ile Gly Lys Lys Lys Ala Asp Leu Met Ala Gln Met Lys		
	740	745 750
Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys		
	755	760 765
Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe		
	770	775 780
Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala		
785	790	795 800
Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr		
	805	810 815
Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys		
	820	825 830
Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val		
	835	840 845
Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg		
	850	855 860
Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg		

865		870		875		880
Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr						
	885			890		895
Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala						
	900			905		910
Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys						
	915			920		925
Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe						
	930			935		940
Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu						
945		950		955		960
Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr						
	965			970		975
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu						
	980			985		990
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu						
	995			1000		1005
Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu						
	1010			1015		1020
Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr						
1025		1030		1035		1040
Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys						
	1045			1050		1055
Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val						
	1060			1065		1070
Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr						
	1075			1080		1085
Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu						
	1090			1095		1100
Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn						
1105		1110		1115		1120
Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu						

1125

1130

1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
 1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile
 1155 1160

<210> 119

<211> 2408

<212> DNA

<213> Aquifex aeolicus

<400> 119

```

atgaactacg ttcccttcgc gagaaagtac agaccgaaat tcttcaggga agtaatagga 60
caggaagctc ccgtaaggat actcaaaaac gctataaaaa acgacagagt ggctcacgcc 120
tacctctttg ccggaccgag ggggggttggg aagacgacta ttgcaagaat tctcgcaaaa 180
gctttgaact gtaaaaatcc ctccaaaggt gagccctgcg gtgagtgcga aaactgcagg 240
gagatagaca ggggtgtggt ccctgactta attgaaatgg atgccgcctc aaacaggggt 300
atagacgacg taagggcatt aaaagaagcg gtcaattaca aacctataaa aggaaagtac 360
aaggtttaca taatagacga agctcacatg ctcacgaaag aagctttcaa cgctctctta 420
aaaaccctcg aagagccccc tcccagaact gttttcgtcc tttgtaccac ggagtacgac 480
aaaattcttc ccacgatact ctcaaggtgt cagaggataa tcttctcaaa ggtaagaaag 540
gaaaaagtaa tagagtatct aaaaaagata tgtgaaaagg aagggattga gtgcgaagag 600
ggagcccttg aggttctggc tcatgcctct gaaggggtgca tgagggatgc agcctctctc 660
ctggaccagg cgagcgttta cggggaaggc agggtaacaa aagaagtagt ggagaacttc 720
ctcggaattc tcagtcagga aagcgtagg agttttctga aattgcttct gaactcagaa 780
gtggacgaag ctataaagtt cctcagagaa ctctcagaaa agggctacaa cctgaccaag 840
ttttgggaga tgttagaaga ggaagtgaga aacgcaattt tagtaaagag cctgaaaaat 900
cccgaagcg tggttcagaa ctggcaggat tacgaagact tcaaagacta ccctctggaa 960
gccctcctct acgttgagaa cctgataaac aggggtaaag ttgaagcgag aacgagagaa 1020
cccttaagag cttttgaact cgcggtaata aagagcctta tagtcaaaga cataattccc 1080
gtatcccagc tcggaagtgt ggtaaaggaa accaaaaagg aagaaaagaa agttgaagta 1140
aaagaagagc caaaagtaaa agaagaaaaa ccaaaggagc aggaagagga caggttccag 1200
aaagttttta acgctgtgga cggcaaaatc cttaaaagaa tacttgaagg ggcaaaaagg 1260
gaagaaagag acggaaaaat cgtcctaaag atagaagcct cttatctgag aaccatgaaa 1320
aaggaatttg actcactaaa ggagactttt ctttttttag agtttgaacc cgtggaggat 1380
aaaaaaaaac ctcagaagtc cagcgggacg aggctgtttt aaaggtaaag gagctcttca 1440
atgcaaaaat actcaaagta cgaagtaaaa gctaagggtca taaagggtgag aatgcccgtg 1500
gaagagatag ggctgtttta cgcactaata gacggcttgc ccaggtagc actcacgagg 1560
acgaaggaaa agggaaaggg agaagttttc gtttttagcga ctctttataa agtcaaggaa 1620
ttgatggaag ctatggaggg tatgaaaaaa cacataaagg atttagaaat cctcggagag 1680
acggatgagg atttaacttt ttaaagtatg ggtgtatctg agcaaagggt taagctaaaa 1740
acaaacctga aaccgcgagg ggaccagccg aaagccataa aaaaactcct tgaaaaccta 1800
aggaaaggcg taaaagaaca aacacttctc ggagtcacgg gaagcggaaa gacttttact 1860
ctagcaaacg taatagcgaa gtacaacaaa ccaactcttg tggtagttca caacaaaatt 1920
ctcgcggcac agctatacag ggagttttaa gaactattcc ctgaaaacgc tgtagagtac 1980

```

```

tttgtctctt actacgacta ttaccaacct gaagcctaca ttcccgaata agatttatac 2040
atagaaaagg acgcgagtat aaacgaaagc tggaacggtt cagacactcc gccacgatat 2100
ccgttctaga aaggaggac gttatagtag ttgcttcagt ttcttgata tacggactcg 2160
ggaaacctga gcactacgaa aacctgagga taaaactcca aagggaata agactgaact 2220
tgagtaagct cctgaggaaa ctcgttgagc taggatata gagaaatgac ttgcccataa 2280
agagggctac cttctcggtt aggggagacg tggttgagat agtcccttct cacacggaag 2340
attacctcgt gagggtagag ttctgggacg acgaagttga aagaatagtc ctcatggacg 2400
ctctgaac 2408

```

<210> 120

<211> 473

<212> PRT

<213> Aquifex aeolicus

<400> 120

```

Met Asn Tyr Val Pro Phe Ala Arg Lys Tyr Arg Pro Lys Phe Phe Arg
  1              5              10              15

```

```

Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
      20              25              30

```

```

Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
      35              40              45

```

```

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
      50              55              60

```

```

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
      65              70              75              80

```

```

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
      85              90              95

```

```

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
      100             105             110

```

```

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
      115             120             125

```

```

His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
      130             135             140

```

```

Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
      145             150             155             160

```

```

Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
      165             170             175

```


Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
 180 185 190

Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
 195 200 205

Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
 210 215 220

Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
 225 230 235 240

Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
 245 250 255

Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
 260 265 270

Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
 275 280 285

Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
 290 295 300

Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
 305 310 315 320

Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
 325 330 335

Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
 340 345 350

Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
 355 360 365

Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
 370 375 380

Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
 385 390 395 400

Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
 405 410 415

Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
 420 425 430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
 435 440 445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro
 450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe
 465 470

<210> 121
 <211> 1090
 <212> DNA
 <213> Aquifex aeolicus

<400> 121
 atgcgcgtta aggtggacag ggaggagctt gaagaggttc ttaaaaaagc aagagaaagc 60
 acggaaaaaa aagccgcact cccgatactc gcgaacttct tactctccgc aaaagaggaa 120
 aacttaatcg taagggcaac ggacttggaa aactaccttg tagtctccgt aaagggggag 180
 gttgaagagg aaggagaggt ttgcggtccac tctcaaaaac tctacgatat agtcaagaac 240
 ttaaattccg cttacgttta ctttcatacg gaaggtgaaa aactcgtcat aacgggagga 300
 aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360
 gtagaaggag gagaaacact ttcgggaaac cttctcgtta acggaataga aaaggtagag 420
 tacgccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatac 480
 gaggacagaa ttcactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540
 taaacattga aaagagtga gacgagtctt ttgcttactt ctccactccc gagtggaaac 600
 tcgccgttag ctcttggaag gagaattccc ggactacatg agtgtcatcc ctgaggagtt 660
 ttcggcgga gtcttgtttg agacagagga agtcttaaag gttttaaaga ggttgaaggc 720
 ttttaagcga ggaaaagttt ttcccgtgaa gattacctta agcgaaaacc ttgccatctt 780
 tgagttcgcg gatccggagt tcggagaagc gagagaggaa attgaagtgg agtacacggg 840
 agagcccttt gagataggat tcaacggaaa taccttatgg aggcgcttga cgcctacgac 900
 agcgaaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960
 gattacgaaa aggaacctta caagtgcata ataatgccga tgaggggtgta gccatgaaaa 1020
 aagctttaat ctttttattg agcttgagcc ttttaattcc tgcgttttagc gaagccaaac 1080
 ccaagtcttc 1090

<210> 122
 <211> 363
 <212> PRT
 <213> Aquifex aeolicus

<400> 122
 Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Glu Val Leu Lys Lys
 1 5 10 15

Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn

20					25					30						
Phe	Leu	Leu	Ser	Ala	Lys	Glu	Glu	Asn	Leu	Ile	Val	Arg	Ala	Thr	Asp	
35					40					45						
Leu	Glu	Asn	Tyr	Leu	Val	Val	Ser	Val	Lys	Gly	Glu	Val	Glu	Glu	Glu	
50					55					60						
Gly	Glu	Val	Cys	Val	His	Ser	Gln	Lys	Leu	Tyr	Asp	Ile	Val	Lys	Asn	
65					70					75					80	
Leu	Asn	Ser	Ala	Tyr	Val	Tyr	Leu	His	Thr	Glu	Gly	Glu	Lys	Leu	Val	
85					90					95						
Ile	Thr	Gly	Gly	Lys	Ser	Thr	Tyr	Lys	Leu	Pro	Thr	Ala	Pro	Ala	Glu	
100					105					110						
Asp	Phe	Pro	Glu	Phe	Pro	Glu	Ile	Val	Glu	Gly	Gly	Glu	Thr	Leu	Ser	
115					120					125						
Gly	Asn	Leu	Leu	Val	Asn	Gly	Ile	Glu	Lys	Val	Glu	Tyr	Ala	Ile	Ala	
130					135					140						
Lys	Glu	Glu	Ala	Asn	Ile	Ala	Leu	Gln	Gly	Met	Tyr	Leu	Arg	Gly	Tyr	
145					150					155					160	
Glu	Asp	Arg	Ile	His	Phe	Val	Gly	Ser	Asp	Gly	His	Arg	Leu	Ala	Leu	
165					170					175						
Tyr	Glu	Pro	Leu	Gly	Glu	Phe	Ser	Lys	Glu	Leu	Leu	Ile	Pro	Arg	Lys	
180					185					190						
Ser	Leu	Lys	Val	Leu	Lys	Lys	Leu	Ile	Thr	Gly	Ile	Glu	Asp	Val	Asn	
195					200					205						
Ile	Glu	Lys	Ser	Glu	Asp	Glu	Ser	Phe	Ala	Tyr	Phe	Ser	Thr	Pro	Glu	
210					215					220						
Trp	Lys	Leu	Ala	Val	Arg	Leu	Leu	Glu	Gly	Glu	Phe	Pro	Asp	Tyr	Met	
225					230					235					240	
Ser	Val	Ile	Pro	Glu	Glu	Phe	Ser	Ala	Glu	Val	Leu	Phe	Glu	Thr	Glu	
245					250					255						
Glu	Val	Leu	Lys	Val	Leu	Lys	Arg	Leu	Lys	Ala	Leu	Ser	Glu	Gly	Lys	
260					265					270						
Val	Phe	Pro	Val	Lys	Ile	Thr	Leu	Ser	Glu	Asn	Leu	Ala	Ile	Phe	Glu	

275		280		285
Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu				
290		295		300
Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met				
305		310		315
				320
Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr				
	325		330	335
Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu				
	340		345	350
Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val				
355		360		

<210> 123
 <211> 1093
 <212> DNA
 <213> Aquifex aeolicus

<400> 123

gtggaaacca	caatattcca	gttccagaaa	acttttttca	caaaacctcc	gaaggagagg	60
gtcttcgtcc	ttcatggaga	agagcagtat	ctcataagaa	cctttttgtc	taagctgaag	120
gaaaagtacg	gggagaatta	cacggttctg	tgggggggatg	agataagcga	ggaggaattc	180
tacactgccc	tttccgagac	cagtatattc	ggcggttcaa	aggaaaaagc	ggtggtcatt	240
tacaacttcg	gggatttcct	gaagaagctc	ggaaggaaga	aaaaggaaaa	agaaaggcct	300
ataaaaagtcc	tcagaaacgt	aaagagtaac	tacgtattta	tagtgtagca	tgcgaaactc	360
cagaaacagg	aactttcttc	ggaacctctg	aaatccgtag	cgtctttcgg	cggtatagtg	420
gtagcaaaca	ggctgagcaa	ggagaggata	aaacagctcg	tccttaagaa	gttcaaagaa	480
aaagggataa	acgtagaaaa	cgatgccctt	gaataccttc	tccagctcac	gggttacaac	540
ttgatggagc	tcaaacttga	ggttgaaaaa	ctgatagatt	acgcaagtga	aaagaaaatt	600
ttaacactcg	atgaggtaaa	gagagtagcc	ttctcagttc	cagaaaacgt	aaacgtattt	660
gagttcgttg	atttactcct	cttaaaagat	tacgaaaagg	ctcttaaagt	tttggactcc	720
ctcatttcct	tcggaataca	ccccctccag	attatgaaaa	tcctgtcctc	ctatgctcta	780
aaactttaca	ccctcaagag	gcttgaagag	aagggagagg	acctgaataa	ggcgatggaa	840
agcgtgggaa	taaagaacaa	ctttctcaag	atgaagttca	aatcttactt	aaaggcaaac	900
tctaaagagg	acttgaagaa	cctaatacctc	tccctccaga	ggatagacgc	tttttctaaa	960
ctttactttc	aggacacagt	gcagttgctg	gggattttctt	gacctcaaga	ctggagaggg	1020
aagttgtgaa	aaatacttct	catggtggat	aatctttttt	atgaagtttg	cggtttgcgt	1080
ttttcccggg	tct					1093

<210> 124
 <211> 350
 <212> PRT

<213> Aquifex aeolicus

<400> 124

Val	Glu	Thr	Thr	Ile	Phe	Gln	Phe	Gln	Lys	Thr	Phe	Phe	Thr	Lys	Pro
1				5					10					15	
Pro	Lys	Glu	Arg	Val	Phe	Val	Leu	His	Gly	Glu	Glu	Gln	Tyr	Leu	Ile
			20					25					30		
Arg	Thr	Phe	Leu	Ser	Lys	Leu	Lys	Glu	Lys	Tyr	Gly	Glu	Asn	Tyr	Thr
		35					40					45			
Val	Leu	Trp	Gly	Asp	Glu	Ile	Ser	Glu	Glu	Glu	Phe	Tyr	Thr	Ala	Leu
	50					55					60				
Ser	Glu	Thr	Ser	Ile	Phe	Gly	Gly	Ser	Lys	Glu	Lys	Ala	Val	Val	Ile
65					70					75					80
Tyr	Asn	Phe	Gly	Asp	Phe	Leu	Lys	Lys	Leu	Gly	Arg	Lys	Lys	Lys	Glu
				85					90					95	
Lys	Glu	Arg	Leu	Ile	Lys	Val	Leu	Arg	Asn	Val	Lys	Ser	Asn	Tyr	Val
			100					105					110		
Phe	Ile	Val	Tyr	Asp	Ala	Lys	Leu	Gln	Lys	Gln	Glu	Leu	Ser	Ser	Glu
		115					120					125			
Pro	Leu	Lys	Ser	Val	Ala	Ser	Phe	Gly	Gly	Ile	Val	Val	Ala	Asn	Arg
	130					135					140				
Leu	Ser	Lys	Glu	Arg	Ile	Lys	Gln	Leu	Val	Leu	Lys	Lys	Phe	Lys	Glu
145					150					155					160
Lys	Gly	Ile	Asn	Val	Glu	Asn	Asp	Ala	Leu	Glu	Tyr	Leu	Leu	Gln	Leu
				165					170					175	
Thr	Gly	Tyr	Asn	Leu	Met	Glu	Leu	Lys	Leu	Glu	Val	Glu	Lys	Leu	Ile
			180					185					190		
Asp	Tyr	Ala	Ser	Glu	Lys	Lys	Ile	Leu	Thr	Leu	Asp	Glu	Val	Lys	Arg
		195					200					205			
Val	Ala	Phe	Ser	Val	Ser	Glu	Asn	Val	Asn	Val	Phe	Glu	Phe	Val	Asp
	210					215					220				
Leu	Leu	Leu	Leu	Lys	Asp	Tyr	Glu	Lys	Ala	Leu	Lys	Val	Leu	Asp	Ser
225					230					235					240

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
 245 250 255
 Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
 260 265 270
 Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
 275 280 285
 Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
 290 295 300
 Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
 305 310 315 320
 Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
 325 330 335
 Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
 340 345 350

<210> 125
 <211> 1051
 <212> DNA
 <213> Aquifex aeolicus

<400> 125
 atggaaaaag ttttttttggg aaaactccag aaaaccttgc acatacccgaggactcctt 60
 ttttacggca aagaaggaag cggaaagacg aaaacagctt ttgaatttgc aaaaggtatt 120
 ttatgtaagg aaaacgtacc tggggatgcg gaagttgtcc ctcttgcaaa cacgtaaacg 180
 agctggagga agccttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
 cggtaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300
 gagcggacat tacataaaga tagaacagat aagggaagtt aagaactttg cctatgtgaa 360
 gcccgacta agcaggagaa aagtaattat aatagacgac gccacgcga tgacctctca 420
 ggcggcaaac gctcttttaa aggtatttga agagccacct gcggacacca cctttatctt 480
 gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaactt ttcaagtgga 540
 gttcaagggc ttttcagtaa aagagggtat ggaaatagcg aaagtagacg aggaaatagc 600
 gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca aagatatcct 660
 aaacaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720
 attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattggt 780
 atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
 actcttttaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgtagc 900
 cgttcaggcg gattaataaa ccgttattga ttccgtaaca tttaaacctt aatctaaatt 960
 atgagagcct ttgaaggagg tctggtatgg aaaatttgaa gattagatat atagatacga 1020
 ggaagatagg aaccgtgagc ggtgtaaaag t 1051

<210> 126
 <211> 305
 <212> PRT
 <213> Aquifex aeolicus

<400> 126

Met	Glu	Lys	Val	Phe	Leu	Glu	Lys	Leu	Gln	Lys	Thr	Leu	His	Ile	Pro
1				5					10					15	
Gly	Gly	Leu	Leu	Phe	Tyr	Gly	Lys	Glu	Gly	Ser	Gly	Lys	Thr	Lys	Thr
			20					25					30		
Ala	Phe	Glu	Phe	Ala	Lys	Gly	Ile	Leu	Cys	Lys	Glu	Asn	Val	Pro	Trp
		35					40					45			
Gly	Cys	Gly	Ser	Cys	Pro	Ser	Cys	Lys	His	Val	Asn	Glu	Leu	Glu	Glu
	50					55					60				
Ala	Phe	Phe	Lys	Gly	Glu	Ile	Glu	Asp	Phe	Lys	Val	Tyr	Lys	Asp	Lys
65					70					75					80
Asp	Gly	Lys	Lys	His	Phe	Val	Tyr	Leu	Met	Gly	Glu	His	Pro	Asp	Phe
				85					90					95	
Val	Val	Ile	Ile	Pro	Ser	Gly	His	Tyr	Ile	Lys	Ile	Glu	Gln	Ile	Arg
			100					105					110		
Glu	Val	Lys	Asn	Phe	Ala	Tyr	Val	Lys	Pro	Ala	Leu	Ser	Arg	Arg	Lys
		115					120					125			
Val	Ile	Ile	Ile	Asp	Asp	Ala	His	Ala	Met	Thr	Ser	Gln	Ala	Ala	Asn
	130					135					140				
Ala	Leu	Leu	Lys	Val	Leu	Glu	Glu	Pro	Pro	Ala	Asp	Thr	Thr	Phe	Ile
145					150					155					160
Leu	Thr	Thr	Asn	Arg	Arg	Ser	Ala	Ile	Leu	Pro	Thr	Ile	Leu	Ser	Arg
			165					170					175		
Thr	Phe	Gln	Val	Glu	Phe	Lys	Gly	Phe	Ser	Val	Lys	Glu	Val	Met	Glu
			180				185						190		
Ile	Ala	Lys	Val	Asp	Glu	Glu	Ile	Ala	Lys	Leu	Ser	Gly	Gly	Ser	Leu
		195					200					205			
Lys	Arg	Ala	Ile	Leu	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Asn	Lys	Val
	210					215					220				

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
 225 230 235 240
 Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile
 245 250 255
 Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
 260 265 270
 Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
 275 280 285
 Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
 290 295 300
 Asp
 305

<210> 127
 <211> 630
 <212> DNA
 <213> Aquifex aeolicus

<400> 127
 atgaacttcc tgaaaaagtt ccttttactg agaaaagctc aaaagtctcc ttacttcgaa 60
 gagttctacg aagaaatcga tttgaaccag aaggtgaaag atgcaagggt ttagtatttt 120
 gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcgggt 180
 gaggttaaaa acctggaaat agacctctct aaatcttttt acgagatact caaaagtgac 240
 gagataaagg cggcggagat acatggaata accagggag acgttgaaaa gtacggaaag 300
 gaaccaaagg aagtaataata cgactttctg aagtacataa agggaagcgt tctcgttggc 360
 tactacgtga agtttgacgt ctcaactcgtt gagaagtact ccataaagta cttccagtat 420
 ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
 aggagtcttg acgaccttat gaaggaactc ggtgtagaaa taagggaag gcacaacgcc 540
 cttgaagatg cctacataac cgctcttctt ttcctaaagt acgtttaccc gaacagggag 600
 tacagactaa aggatctccc gattttcctt 630

<210> 128
 <211> 210
 <212> PRT
 <213> Aquifex aeolicus

<400> 128
 Met Asn Phe Leu Lys Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser
 1 5 10 15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

20	25	30
Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp		
35	40	45
Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn		
50	55	60
Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp		
65	70	75 80
Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu		
85	90	95
Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr		
100	105	110
Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser		
115	120	125
Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn		
130	135	140
Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly		
145	150	155 160
Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala		
165	170	175
Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu		
180	185	190
Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile		
195	200	205
Phe Leu		
210		

<210> 129

<211> 526

<212> DNA

<213> Aquifex aeolicus

<400> 129

atgctcaata aggtttttat aataggaaga cttacgggtg accccgttat aacttatcta 60
 ccgagcggaa cgcccgtagt agagtttact ctggcttaca acagaaggta taaaaaccag 120
 aacggtgaat ttcaggagga aagtcacttc tttgacgtaa aggcgtacgg aaaaatggct 180

```

gaagactggg ctacacgctt ctcgaaagga tacctcgtag tcgtagaggg aagactctcc 240
caggaaaagt gggagaaaga aggaaagaag ttctcaaagg tcaggataat agcggaaaac 300
gtaagattaa taaacaggcc gaaagggtgct gaacttcaag cagaagaaga ggaggaagtt 360
cctcccattg aggaggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataccttt ttaattttga ggagggttaa gtatggtagt gagagctcct 480
aagaagaaag tttgtatgta ctgtgaacaa aagagagagc cagatt 526

```

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

```

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
  1             5             10             15

```

```

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
      20             25             30

```

```

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
      35             40             45

```

```

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
      50             55             60

```

```

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
      65             70             75             80

```

```

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
      85             90             95

```

```

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
      100            105            110

```

```

Gln Ala Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
      115            120            125

```

```

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
      130            135            140

```

```

Ile Pro Phe
145

```

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

```
atgcaatttg tggataaact tccctgtgac gaatccgccg agagggcggt tcttggcagt 60
atgcttgaag accccgaaaa catacctctg gtacttgaat accttaaaga agaagacttc 120
tgcatagacg agcacaagct acttttcagg gttcttacia acctctgggtc cgagtacggc 180
aataagctcg atttcgtatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240
atacctatag actggctcga agaactctac gaggaggcgg tatcccctga cacgcttgag 300
gaagtctgca aaatagtaaa acaacgttcc gcacagaggg cgataattca actcgggtata 360
gaactcattc acaaaggaaa ggaaaacaaa gactttcaca cattaatcga ggaagcccag 420
agcaggatat tttccatagc ggaaagtgtc acatctacgc agttttacca tgtgaaagac 480
gttgcggaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcggtttcac ggaactcgat ctaaagacga cgggattcca ccctggagac 600
ttaataatac tcgccgcaag acccggtatg gggaaaaccg cttttatgct ctccataatc 660
tacaatctcg caaaagacga gggaaaaccc tcagctgtat tttccttgga aatgagcaag 720
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tctggaagta tategaatga agatttaaaag aagcttgaag caagcgcaat agaactcgca 840
aagtacgaca tatacctcga cgacacaccc gctctcacta caacggattt aaggataagg 900
gcaagaaagc tcagaaagga aaaggaagtt gagttcgtgg cgggtggacta cttgcaactt 960
ctgagaccgc cagtccgaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
ttaaaagccc ttgcaaagga acttcacatt cccgttatgg cacttgcgca gctctcccgt 1080
gaggtggaaa agaggagtga taaaagaccc cagcttgagg acctcagaga atccggacag 1140
atagaacagg acgcagacct aatccttttc ctccacagac ccgagtacta caagaaaaag 1200
ccaaatcccg aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260
acggacattg tgaagctcgc atttattaag gagtacacta agtttgcaaa cctagaagcc 1320
cttcctgaac aacctcctga agaagaggaa ctttccgaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttggctatc 1440
cggggtagct caatcggcag agcgggtggc tg 1472
```

<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

```
Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
  1                      5                      10                     15

Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
          20                      25                     30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
          35                      40                     45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
          50                      55                     60
```

Phe	Val	Leu	Ile	Lys	Asp	His	Leu	Glu	Lys	Lys	Asn	Leu	Leu	Gln	Lys	65	70	75	80
Ile	Pro	Ile	Asp	Trp	Leu	Glu	Glu	Leu	Tyr	Glu	Glu	Ala	Val	Ser	Pro	85	90	95	
Asp	Thr	Leu	Glu	Glu	Val	Cys	Lys	Ile	Val	Lys	Gln	Arg	Ser	Ala	Gln	100	105	110	
Arg	Ala	Ile	Ile	Gln	Leu	Gly	Ile	Thr	Ser	Thr	Gln	Phe	Tyr	His	Val	115	120	125	
Lys	Asp	Val	Ala	Glu	Glu	Val	Ile	Glu	Leu	Ile	Tyr	Lys	Phe	Lys	Ser	130	135	140	
Ser	Asp	Arg	Leu	Val	Thr	Gly	Leu	Pro	Ser	Gly	Phe	Thr	Glu	Leu	Asp	145	150	155	160
Leu	Lys	Thr	Thr	Gly	Phe	His	Pro	Gly	Asp	Leu	Ile	Ile	Leu	Ala	Ala	165	170	175	
Arg	Pro	Gly	Met	Gly	Lys	Thr	Ala	Phe	Met	Leu	Ser	Ile	Ile	Tyr	Asn	180	185	190	
Leu	Ala	Lys	Asp	Glu	Gly	Lys	Pro	Ser	Ala	Val	Phe	Ser	Leu	Glu	Met	195	200	205	
Ser	Lys	Glu	Gln	Leu	Val	Met	Arg	Leu	Leu	Ser	Met	Met	Ser	Glu	Val	210	215	220	
Pro	Leu	Phe	Lys	Ile	Arg	Ser	Gly	Ser	Ile	Ser	Asn	Glu	Asp	Leu	Lys	225	230	235	240
Lys	Leu	Glu	Ala	Ser	Ala	Ile	Glu	Leu	Ala	Lys	Tyr	Asp	Ile	Tyr	Leu	245	250	255	
Asp	Asp	Thr	Pro	Ala	Leu	Thr	Thr	Thr	Asp	Leu	Arg	Ile	Arg	Ala	Arg	260	265	270	
Lys	Leu	Arg	Lys	Glu	Lys	Glu	Val	Glu	Phe	Val	Ala	Val	Asp	Tyr	Leu	275	280	285	
Gln	Leu	Leu	Arg	Pro	Pro	Val	Arg	Lys	Ser	Ser	Arg	Gln	Glu	Glu	Val	290	295	300	
Ala	Glu	Val	Ser	Arg	Asn	Leu	Lys	Ala	Leu	Ala	Lys	Glu	Leu	His	Ile	305	310	315	320

Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser
325 330 335

Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu
340 345 350

Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys
355 360 365

Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala
370 375 380

Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys
385 390 395 400

Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro
405 410 415

Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly
420 425 430

Phe Glu Asp Ile Asp Phe
435

<210> 133
<211> 1526
<212> DNA
<213> Aquifex aeolicus

<400> 133
atgtcctcgg acatagacga acttagacgg gaaatagata tagtagacgt catttccgaa 60
tacttaaact tagagaaggt aggttccaat tacagaacga actgtccctt tcaccctgac 120
gatacaccct ccttttacgt gtctccaagt aaacaaatat tcaagtgttt cggttgcggg 180
gtagggggag acgcgataaa gttcgtttcc ctttacgagg acatctccta ttttgaagcc 240
gcccttgaac tcgcaaaacg ctacggaaag aaattagacc ttgaaaagat atcaaaagac 300
gaaaaggtat acgtggctct tgacagggtt tgtgatttct acagggaaag ccttctcaaa 360
aacagagagg caagtgagta cgtaaagagt aggggaatag accctaaagt agcgaggaag 420
tttgatcttg ggtacgcacc ttccagtga gacactcgtaa aagtcttaaa agagaacgat 480
cttttagagg cttaccttga aactaaaaac ctcttttctc ctacgaaggg tgtttacagg 540
gatctctttc ttcggcgtgt cgtgatcccg ataaaggatc cgaggggaag agttataggt 600
ttcgggtggaa ggaggatagt agaggacaaa tctcccaagt acataaactc tccagacagc 660
agggtattta aaaaggggga gaacttattc ggtctttacg aggcaaagga gtatataaag 720
gaagaaggat ttgcgatact tgtggaaggg tactttgacc ttttgagact tttttccgag 780
ggaataagga acgttgttgc acccctcggg acagccctga cccaaaatca ggcaaaccctc 840
ctttccaagt tcacaaaaaa ggtctacatc ctttacgacg gagatgatgc gggaagaaag 900
gctatgaaaa gtgccattcc cctactcctc agtgcaggag tggaagttta tcccgtttac 960
ctccccgaag gatacgatcc cgacgagttt ataaaggaat tcgggaaaga ggaattaaga 1020

```

agactgataa acagctcagg ggagctcttt gaaacgctca taaaaaccgc aagggaaaac 1080
ttagaggaga aaacgcgtga gttcaggtat tatctgggct ttatttccga tggagtaagg 1140
cgctttgctc tggcttcgga gtttcacacc aagtacaaag ttcctatgga aattttatta 1200
atgaaaattg aaaaaaattc tcaagaaaaa gaaattaaac tctcctttaa ggaaaaaatc 1260
ttcctgaaag gactgataga attaaaacca aaaatagacc ttgaagtcct gaacttaagt 1320
cctgagttaa aggaactcgc agttaacgcc ttaaaccggag aggagcattt acttccaaaa 1380
gaagttctcg agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440
ttacaaaaat ctgggaaaaa gaggaagaaa agaggggttg aaaatgtaaa tacttaatta 1500
actttaataa attttttagag ttagga                                     1526

```

<210> 134
 <211> 498
 <212> PRT
 <213> Aquifex aeolicus

```

<400> 134
Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
  1              5              10              15

Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
      20              25              30

Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
      35              40              45

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
      50              55              60

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
      65              70              75              80

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
      85              90              95

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
      100             105             110

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
      115             120             125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
      130             135             140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
      145             150             155             160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

```

	165		170		175
Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys					
	180		185		190
Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu					
	195		200		205
Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys					
	210		215		220
Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys					
	225		230		240
Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg					
	245		250		255
Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala					
	260		265		270
Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val					
	275		280		285
Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser					
	290		295		300
Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr					
	305		310		320
Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys					
	325		330		335
Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr					
	340		345		350
Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe					
	355		360		365
Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu					
	370		375		380
Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu					
	385		390		400
Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe					
	405		410		415
Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile					

420	425	430
Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val		
435	440	445
Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu		
450	455	460
Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp		
465	470	480
Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val		
485	490	495

Asn Thr

<210> 135
 <211> 705
 <212> DNA
 <213> Aquifex aeolicus

<400> 135
 atgcaagata cgcctacctg cagtatttgt caggggacgg gattcgtaaa gaccgaagac 60
 aacaaggtaa ggctctgcga atgcaggttc aagaaaaggg atgtaaacag ggaactaaac 120
 atcccaaaga ggtactggaa cgccaactta gacacttacc accccaagaa cgtatcccag 180
 aacagggcac ttttgacgat aaggggtcttc gtccacaact tcaatcccga ggaagggaaa 240
 gggcttacct ttgtaggatc tcctggagtc ggcaaaaactc accttgcggt tgcaacatta 300
 aaagcgattt atgagaagaa gggaatcaga ggatacttct tcgatacgaa ggatctaata 360
 ttcagggttaa aacacttaat ggacgagggg aaggatacaa agttttttaa aactgtctta 420
 aactcaccgg ttttggttct cgacgacctc gggtctgaga ggctcagtga ctggcagagg 480
 gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540
 acgaattact cactccagag ggaagaagag agtagcgtga ggataagtgc ggatcttgca 600
 agcagactcg gagaaaacgt agtttcaaaa atttacgaga tgaacgagtt gctcgttata 660
 aagggttccg acctcaggaa gtctaataaag ctatcaaccc catct 705

<210> 136
 <211> 235
 <212> PRT
 <213> Aquifex aeolicus

<400> 136
 Met Gln Asp Thr Ala Thr Cys Ser Ile Cys Gln Gly Thr Gly Phe Val
 1 5 10 15
 Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys

atgaaaaaga	ttgaaaat	gaagtggaaa	aatgtctcgt	ttaaaagcct	ggaaatagat	60
cccgatgcag	gtgtggttct	cgtttccgtg	gaaaaattct	ccgaagagat	agaagacctt	120
gtgcgtttac	tggagaagaa	gacgcggttt	cgagtcacgc	tgaacggtgt	tcaaaaaagt	180
aacggggatc	taaggggaaa	gatactttcc	cttctcaacg	gtaatgtgcc	ttacataaaa	240
gatgttggtt	tcgaaggaaa	caggctgatt	ctgaaagtgc	ttggagattt	cgcgcgggac	300
aggatcgcct	ccaaactcag	aagcacgaaa	aaacagctcg	atgaactgct	gcctcccgga	360
acagagatca	tgctggaggt	tgtggagcct	ccggaagatc	ttttgaaaaa	ggaagtacca	420
caaccagaaa	agagagaaga	accaaagggg	gaagaattga	agatcgagga	tgaaaaccac	480
atctttggac	agaaacccag	aaagatcgtc	ttcaccccct	caaaaatctt	tgagtacaac	540
aaaaagacat	cgggtgaagg	caagatcttc	aaaatagaga	agatcgaggg	gaaaagaacg	600
gtccttctga	tttacctgac	agacggagaa	gatttctctga	tctgcaaagt	cttcaacgac	660
gttgaaaagg	tcgaagggaa	agtatcgggtg	ggagacgtga	tcgttgccac	aggagacctc	720
cttctcgaaa	acgggggagcc	caccctttac	gtgaagggaa	tcacaaaact	tcccgaagcg	780
aaaaggatgg	acaaatctcc	ggttaagagg	gtggagctcc	acgcccatac	caagttcagc	840
gatcaggacg	caataacaga	tgtgaacgaa	tatgtgaaac	gagccaagga	atggggcttt	900
cccgcgatag	ccctcacgga	tcatgggaac	gttcaggcca	taccttactt	ctacgacgcg	960
gcgaaagaag	ctggaataaa	gcccattttc	ggtatcgaag	cgtatctggt	gagtgcggtg	1020
gagcccgtca	taaggaatct	ctccgacgat	tcgacgtttg	gagatgccac	gttcgtcgtc	1080
ctcgacttcg	agacgacggg	tctcgacccg	caggtggatg	agatcatcga	gataggagcg	1140
gtgaagatac	agggtggcca	gatagtggac	gagtaccaca	ctctcataaa	gccttccagg	1200
gagatctcaa	gaaaaagttc	ggagatcacc	ggaatcactc	aagagatgct	ggaaaacaag	1260
agaagcatcg	aggaagtctt	gccggagttc	ctcgggtttc	tggaagattc	catcatcgta	1320
gcacacaacg	ccaacttcga	ctacagattt	ctgaggctgt	ggatcaaaaa	agtgatggga	1380
ttggactggg	aaagacccta	catagatacg	ctcgccctcg	caaagtcctt	tctcaaactg	1440
agaagctact	ctctggattc	cgttgtggaa	aagctcggat	tgggtccctt	ccggcaccac	1500
agggccctgg	atgacgcgag	ggtcacccgt	caggttttcc	tcaggttcgt	tgagatgatg	1560
aagaagatcg	gtatcacgaa	gctttcagaa	atggagaagt	tgaaggatac	gatagactac	1620
accgcgttga	aacccttcca	ctgcacgata	ctcgttcaga	acaaaaaggg	attgaaaaac	1680
ctatacaaac	tggtttctga	ttcctatata	aagtacttct	acggtgttcc	gaggatcctc	1740
aaaagtgagc	tcatcgagaa	cagagaagga	ctgctcgtgg	gtagcgcggtg	tatctccggt	1800
gagctcggac	gtgccgccct	cgaaggagcg	agtgattcag	aactcgaaga	gatcgcgag	1860
ttctacgact	acatagaagt	catgccgctc	gacgttatag	ccgaagatga	agaagacctt	1920
gacagagaaa	gactgaaaga	agtgtaccga	aaactctaca	gaatagcgaa	aaaattgaac	1980
aagttcgtcg	tcatgaccgg	tgatgttcat	ttcctcgatc	ccgaagatgc	caggggcaga	2040
gctgcacttc	tggcacctca	gggaaacaga	aacttcgaga	atcagcccgc	actctacctc	2100
agaacgaccg	aagaaatgct	cgagaaggcg	atagagatat	tcgaagatga	agagatcgcg	2160
agggaagtcg	tgatagagaa	tcccaacaga	atagccgata	tgatcgagga	agtgcagccg	2220
ctcgagaaaa	aacttcaccc	gccgatcata	gagaacgccg	atgaaatagt	gagaaacctc	2280
accatgaagc	gggcgtacga	gatctacggt	gatccgcttc	ccgaaatcgt	ccagaagcgt	2340
gtggaaaagg	aactgaacgc	catcataaat	catggatacg	ccgttctcta	tctcatcgct	2400
caggagctcg	ttcagaaatc	tatgagcgat	ggttacgtgg	ttggatccag	aggatccgtc	2460
gggtcttcac	tcgtggccaa	tctcctcgga	ataacagagg	tgaatcccct	accaccacat	2520
tacaggtgtc	cagagtgcaa	atactttgaa	gttgtcgaag	acgacagata	cggagcgggt	2580
tacgaccttc	ccaacaagaa	ctgtccaaga	tgtggggctc	ctctcagaaa	agacggccac	2640
ggcataccgt	ttgaaacgtt	catgggggttc	gagggtgaca	aggccccga	catagatctc	2700
aacttctcag	gagagtatca	ggaacgtgct	catcgttttg	tggaagaact	cttcggtaaa	2760
gaccacgtct	atagggcggg	aaccataaac	accatcgcg	aaagaagtgc	ggtgggttac	2820
gtgagaagct	acgaagagaa	aaccggaaaag	aagctcagaa	aggcggaaat	ggaaagactc	2880

```

gtttccatga tcacgggagt gaagagaacg acgggtcagc acccaggggg gctcatgac 2940
ataccgaaag acaaagaagt ctacgatttc actcccatac agtatccagc caacgataga 3000
aacgcaggtg tggtcaccac gcacttcgca tacgagacga tccatgatga cctggtgaag 3060
atagatgcgc tcggccacga tgatcccact ttcatacaaga tgctcaagga cctcaccgga 3120
atcgatccca tgacgattcc catggatgac cccgatacgc tcgccatatt cagttctgtg 3180
aagcctcttg gtgtggatcc cgttgagctg gaaagcgatg tgggaacgta cggaattccg 3240
gagttcggaa ccgagtttgt gaggggaatg ctcgttgaaa cgagaccaa gagtttcgcc 3300
gagcttgtga gaatctcagg actgtcacac ggtacggacg tctggttgaa caacgcacgt 3360
gattggataa acctcggcta cgccaagctc tccgagggtta tctcgtgtag ggacgacatc 3420
atgaacttcc tcatacacia aggaatggaa ccgtcacttg cttcaagat catggaaaac 3480
gtcaggaagg gaaagggtat cacagaagag atggagagcg agatgagaag gctgaagggt 3540
ccagaatggt tcatcgaatc ctgtaaaagg atcaaatac tcttcccga agctcacgct 3600
gtggcttacg tgagtatggc cttcagaatt gcttacttca aggttacta tcctcttcag 3660
ttttacgcgg cgtacttcac gataaaagg gatcagttcg atccggttct cgtactcagg 3720
ggaaaagaag ccataaagag gcgcttgaga gaactcaaag cgatgcctgc caaagacgcc 3780
cagaagaaaa acgaagtgag tgttctggag gttgccctgg aaatgatact gagaggtttt 3840
tccttcctac cgcccagacat cttcaaatac gacgcgaaga aatttctgat agaaggaaac 3900
tcgctgagaa ttccgttcaa caaacttcca ggactgggtg acagcggtgc cgagtcgata 3960
atcagagcca gggaagaaaa gccgttact tcggtggaag atctcatgaa gaggaccaag 4020
gtcaacaaaa atcacataga gctgatgaaa agcctgggtg ttctcgggga cttccagag 4080
acggaacagt tcacgctttt c 4101

```

<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

```

Met Lys Lys Ile Glu Asn Leu Lys Trp Lys Asn Val Ser Phe Lys Ser
  1                      5                      10                      15

```

```

Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
          20                      25                      30

```

```

Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
          35                      40                      45

```

```

Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
          50                      55                      60

```

```

Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
          65                      70                      75                      80

```

```

Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
          85                      90                      95

```

```

Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln

```

100	105	110
Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val		
115	120	125
Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys		
130	135	140
Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His		
145	150	155
Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile		
	165	170
Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile		
	180	185
Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp		
	195	200
Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val		
	210	215
Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu		
225	230	235
Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys		
	245	250
Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu		
	260	265
Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val		
	275	280
Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala		
	290	295
Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala		
305	310	315
Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu		
	325	330
Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr		
	340	345
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu		

355		360		365
Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln				
370		375		380
Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg				
385		390		395 400
Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met				
	405		410	415
Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly				
	420		425	430
Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr				
	435		440	445
Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu				
	450		455	460
Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu				
	465		470	475 480
Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro				
	485		490	495
Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val				
	500		505	510
Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu				
	515		520	525
Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys				
	530		535	540
Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn				
	545		550	555 560
Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val				
	565		570	575
Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu				
	580		585	590
Val Gly Ser Ala Cys Ile Ser Gly Glu Leu Gly Arg Ala Ala Leu Glu				
	595		600	605
Gly Ala Ser Asp Ser Glu Leu Glu Glu Ile Ala Lys Phe Tyr Asp Tyr				

610		615		620	
Ile Glu Val Met Pro Leu Asp Val Ile Ala Glu Asp Glu Glu Asp Leu					
625		630		635	640
Asp Arg Glu Arg Leu Lys Glu Val Tyr Arg Lys Leu Tyr Arg Ile Ala					
	645		650		655
Lys Lys Leu Asn Lys Phe Val Val Met Thr Gly Asp Val His Phe Leu					
	660		665		670
Asp Pro Glu Asp Ala Arg Gly Arg Ala Ala Leu Leu Ala Pro Gln Gly					
	675		680		685
Asn Arg Asn Phe Glu Asn Gln Pro Ala Leu Tyr Leu Arg Thr Thr Glu					
	690		695		700
Glu Met Leu Glu Lys Ala Ile Glu Ile Phe Glu Asp Glu Glu Ile Ala					
705		710		715	720
Arg Glu Val Val Ile Glu Asn Pro Asn Arg Ile Ala Asp Met Ile Glu					
	725		730		735
Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn					
	740		745		750
Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile					
	755		760		765
Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu					
	770		775		780
Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala					
785		790		795	800
Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser					
	805		810		815
Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr					
	820		825		830
Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr					
	835		840		845
Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro					
850		855		860	
Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His					

865		870		875		880
Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro						
	885			890		895
Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg						
	900			905		910
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr						
	915			920		925
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr						
	930			935		940
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu						
945		950		955		960
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly						
	965			970		975
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro						
	980			985		990
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His						
	995			1000		1005
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu						
1010		1015		1020		
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly						
1025		1030		1035		1040
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile						
	1045			1050		1055
Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser						
	1060			1065		1070
Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg						
	1075			1080		1085
Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg						
1090		1095		1100		
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg						
1105		1110		1115		1120
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys						

1125	1130	1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser		
1140	1145	1150
Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr		
1155	1160	1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe		
1170	1175	1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala		
1185	1190	1195 1200
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His		
1205	1210	1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln		
1220	1225	1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg		
1235	1240	1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn		
1250	1255	1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe		
1265	1270	1275 1280
Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu		
1285	1290	1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu		
1300	1305	1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro		
1315	1320	1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn		
1330	1335	1340
His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu		
1345	1350	1355 1360
Thr Glu Gln Phe Thr Leu Phe		
1365		

<210> 139
 <211> 567
 <212> DNA
 <213> *Thermatoga maritima*

<400> 139
 gtgctcgcca tgatatggaa cgacaccggt ttttgcgctg tagacacaga aaccacggga 60
 accgatccct ttgccggaga ccggatagtt gaaatagccg ctgttcctgt cttcaagggg 120
 aagatctaca gaaacaaagc gtttcactct ctcgatgaat ccagaataag aatccctgcg 180
 ctgattcaga aagttcacgg tatcagcaac atggacatcg tggaagcgcc agacatggac 240
 acagtttacg atctttttcag ggattacgtg aagggaacgg tgctcgtgtt tcacaacgcc 300
 aacttcgacc tcactttttct ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360
 aatccctaca tcgacacact cgatctttca gaagagatct ttggaaggcc tcattctctc 420
 aaatggctct ccgaaagact tggaataaaa accacgatac ggcaccgtgc tcttccagat 480
 gccctggtga ccgcaagagt ttttgtgaag cttgttgaat ttcttggtga aaacagggtc 540
 aacgaattca tacgtggaaa acggggg 567

<210> 140
 <211> 189
 <212> PRT
 <213> *Thermatoga maritima*

<400> 140
 Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr
 1 5 10 15
 Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
 20 25 30
 Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
 35 40 45
 His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
 50 55 60
 Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
 65 70 75 80
 Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
 85 90 95
 Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
 100 105 110
 Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
 115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
 130 135 140
 Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
 145 150 155 160
 Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
 165 170 175
 Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
 180 185

<210> 141
 <211> 1434
 <212> DNA
 <213> *Thermatoga maritima*

<400> 141
 gtggaagttc ttacaggaa gtacaggcca aagacttttt ctgaggttgt caatcaggat 60
 catgtgaaga aggcaataat cgggtgctatt cagaagaaca gcgtggccca cggatacata 120
 ttcgccggtc cgaggggaac ggggaagact actcttgcca gaattctcgc aaaatccctg 180
 aactgtgaga acagaaagg agttgaaccc tgcaattcct gcagagcctg cagagagata 240
 gacgaggga ccttcattga cgtgatagag ctcgacgcgg cctccaacag aggaatagac 300
 gagatcagaa gaatcagaga cgccgttgga tacaggccga tgggaaggtaa atacaaagtc 360
 tacataatag acgaagttca catgctcacg aaagaagcct tcaacgcgct cctcaaaaca 420
 ctcgaagaac ctcttccca cgtcgtgttc gtgctggcaa cgacaaacct tgagaagggt 480
 cctcccacga ttatctcgag atgtcagggt ttcgagttca gaaacattcc cgacgagctc 540
 atcgaaaaga ggctccagga agttgcggag gctgaaggaa tagagataga cagggaagct 600
 ctgagcttca tcgcaaaaag agcctctgga ggcttgagag acgcgctcac catgctcgag 660
 cagggtgtgga agttctcgga aggaagata gatctcgaga cggtagacag ggcgctcggg 720
 ttgataccga tacagggtgt tcgcgattac gtgaacgcta tcttttctgg tgatgtgaaa 780
 agggctcttca ccgttctcga cgacgtctat tacagcgagg aggactacga ggtgctcatt 840
 caggaagcag tcgaggatct ggtcgaagac ctggaaagg agagaggggt ttaccagggt 900
 tcagcgaacg atatagttca ggtttcggaga caacttctga atcttctgag agagataaag 960
 ttcgccgaag aaaaacgact cgtctgtaaa gtgggttcgg cttacatagc gacgaggttc 1020
 tccaccacaa acgttcagga aaacgatgtc agagaaaaaa acgataattc aaatgtacag 1080
 cagaaagaag agaagaaaga aacggtgaag gcaaaagaag aaaaacagga agacagcgag 1140
 ttcgagaaac gcttcaaaga actcatggaa gaactgaaag aaaagggcga tctctctatc 1200
 tttgtcgctc tcagcctctc agaggtgcag tttgacggag aaaagggtgat tatttctttt 1260
 gattcatcga aagctatgca ttacgagttg atgaagaaaa aactgcctga gctggaaaac 1320
 attttttcta gaaaactcgg gaaaaaagta gaagttgaac ttcgactgat gggaaaagaa 1380
 gaaacaatcg agaaggtttc tcagaagatc ctgagattgt ttgaacagga ggga 1434

<210> 142
 <211> 478
 <212> PRT

<213> *Thermatoga maritima*

<400> 142

Met Glu Val Leu Tyr Arg Lys Tyr Arg Pro Lys Thr Phe Ser Glu Val
1 5 10 15

Val Asn Gln Asp His Val Lys Lys Ala Ile Ile Gly Ala Ile Gln Lys
20 25 30

Asn Ser Val Ala His Gly Tyr Ile Phe Ala Gly Pro Arg Gly Thr Gly
35 40 45

Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ser Leu Asn Cys Glu Asn
50 55 60

Arg Lys Gly Val Glu Pro Cys Asn Ser Cys Arg Ala Cys Arg Glu Ile
65 70 75 80

Asp Glu Gly Thr Phe Met Asp Val Ile Glu Leu Asp Ala Ala Ser Asn
85 90 95

Arg Gly Ile Asp Glu Ile Arg Arg Ile Arg Asp Ala Val Gly Tyr Arg
100 105 110

Pro Met Glu Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Val His Met
115 120 125

Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro
130 135 140

Pro Ser His Val Val Phe Val Leu Ala Thr Thr Asn Leu Glu Lys Val
145 150 155 160

Pro Pro Thr Ile Ile Ser Arg Cys Gln Val Phe Glu Phe Arg Asn Ile
165 170 175

Pro Asp Glu Leu Ile Glu Lys Arg Leu Gln Glu Val Ala Glu Ala Glu
180 185 190

Gly Ile Glu Ile Asp Arg Glu Ala Leu Ser Phe Ile Ala Lys Arg Ala
195 200 205

Ser Gly Gly Leu Arg Asp Ala Leu Thr Met Leu Glu Gln Val Trp Lys
210 215 220

Phe Ser Glu Gly Lys Ile Asp Leu Glu Thr Val His Arg Ala Leu Gly
225 230 235 240

Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser
 245 250 255
 Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser
 260 265 270
 Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val
 275 280 285
 Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp
 290 295 300
 Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys
 305 310 315 320
 Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile
 325 330 335
 Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu
 340 345 350
 Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr
 355 360 365
 Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg
 370 375 380
 Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile
 385 390 395 400
 Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val
 405 410 415
 Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys
 420 425 430
 Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys
 435 440 445
 Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu
 450 455 460
 Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly
 465 470 475

<210> 143

<211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

```
atgaaagtaa ccgtcacgac tcttgaattg aaagacaaaa taaccatcgc ctcaaaagcg 60
ctcgcaaaga aatccgtgaa acccattctt gctggatttc ttttcgaagt gaaagatgga 120
aatttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggta ccaggagatg tcattcagaa gatggtcaag 240
gttctcccag atgagataac ggaactttct ttagaggggg atgctcttgt tataagttct 300
ggaagcacccg ttttcaggat caccaccatg cccgcggacg aatttccaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat gggtgaaaag 420
gtcatcttcg ccgctgccaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatggtt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggta cgatggaaga 660
agggtttctc tgctgacaaa tgatgtagaa acggtgatga gagtggtcga cgctgaattt 720
cccgattaca aaagggatgat ccccgaaact ttcaaaacga aagtgggtgg ttccagaaaa 780
gaactcaggg aatctttgaa gagggatgat gtgattgcca gcaagggaag cgagtccgtg 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagcccgga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaagaa ggggaagatc tcgtgatcgc tttcaaccgc 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagtg 1080
atgccccatca gactggca                                     1098
```

<210> 144

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

```
Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
  1                      5                      10                      15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
          20                      25                      30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
          35                      40                      45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
          50                      55                      60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
          65                      70                      75                      80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
          85                      90                      95
```

Val	Ile	Ser	Ser	Gly	Ser	Thr	Val	Phe	Arg	Ile	Thr	Thr	Met	Pro	Ala			
			100					105					110					
Asp	Glu	Phe	Pro	Glu	Ile	Thr	Pro	Ala	Glu	Ser	Gly	Ile	Thr	Phe	Glu			
		115					120					125						
Val	Asp	Thr	Ser	Leu	Leu	Glu	Glu	Met	Val	Glu	Lys	Val	Ile	Phe	Ala			
	130					135					140							
Ala	Ala	Lys	Asp	Glu	Phe	Met	Arg	Asn	Leu	Asn	Gly	Val	Phe	Trp	Glu			
145					150					155					160			
Leu	His	Lys	Asn	Leu	Leu	Arg	Leu	Val	Ala	Ser	Asp	Gly	Phe	Arg	Leu			
			165					170						175				
Ala	Leu	Ala	Glu	Glu	Gln	Ile	Glu	Asn	Glu	Glu	Glu	Ala	Ser	Phe	Leu			
			180					185					190					
Leu	Ser	Leu	Lys	Ser	Met	Lys	Glu	Val	Gln	Asn	Val	Leu	Asp	Asn	Thr			
		195					200					205						
Thr	Glu	Pro	Thr	Ile	Thr	Val	Arg	Tyr	Asp	Gly	Arg	Arg	Val	Ser	Leu			
	210					215					220							
Ser	Thr	Asn	Asp	Val	Glu	Thr	Val	Met	Arg	Val	Val	Asp	Ala	Glu	Phe			
225					230					235					240			
Pro	Asp	Tyr	Lys	Arg	Val	Ile	Pro	Glu	Thr	Phe	Lys	Thr	Lys	Val	Val			
			245						250					255				
Val	Ser	Arg	Lys	Glu	Leu	Arg	Glu	Ser	Leu	Lys	Arg	Val	Met	Val	Ile			
			260					265					270					
Ala	Ser	Lys	Gly	Ser	Glu	Ser	Val	Lys	Phe	Glu	Ile	Glu	Glu	Asn	Val			
		275					280					285						
Met	Arg	Leu	Val	Ser	Lys	Ser	Pro	Asp	Tyr	Gly	Glu	Val	Val	Asp	Glu			
	290					295					300							
Val	Glu	Val	Gln	Lys	Glu	Gly	Glu	Asp	Leu	Val	Ile	Ala	Phe	Asn	Pro			
305					310					315					320			
Lys	Phe	Ile	Glu	Asp	Val	Leu	Lys	His	Ile	Glu	Thr	Glu	Glu	Ile	Glu			
			325					330						335				
Met	Asn	Phe	Val	Asp	Ser	Thr	Ser	Pro	Cys	Gln	Ile	Asn	Pro	Leu	Asp			
			340					345					350					

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
 355 360 365

<210> 145
 <211> 972
 <212> DNA
 <213> *Thermatoga maritima*

<400> 145
 atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60
 ctctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
 gatttcataa ggtctttact caggacaaag acgatctttt ccaacaagac gatcattgac 180
 atcgtcaatt tcgatgagtg gaaagcacag gagcagaagc gtctcggtga acttttgaaa 240
 aacgtaccgg aagacgttca tatcttcatc cgttctcaaa aaacaggtgg aaagggagta 300
 gcgctggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360
 ttcagggaga atggtttgct catcgataaa gatgcccttc agctgttttt ctccaagggt 420
 ggaacgaacg acctgatcat agaaagggag attgaaaaac tgaaagctta ttccgaggac 480
 agaaagataa cggtagaaga cgtggaagag gtcgttttta cctatcagac tccgggatac 540
 gatgattttt gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600
 cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcaacttcttg 660
 gatctcttca aaatcctcgt tcttgtgaca aagaaaagat actacacctg gcctgatgtg 720
 tccagggtgt ccaaagagct gggaattccc gttcctcgtg tggctcgttt cctcgggtttc 780
 tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
 gttagaaga tactgaggga tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
 ccaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960
 agagatgaag aa 972

<210> 146
 <211> 324
 <212> PRT
 <213> *Thermatoga maritima*

<400> 146
 Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
 1 5 10 15
 Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
 20 25 30
 His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
 35 40 45
 Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
 50 55 60

Asp	Glu	Trp	Lys	Ala	Gln	Glu	Gln	Lys	Arg	Leu	Val	Glu	Leu	Leu	Lys	65	70	75	80
Asn	Val	Pro	Glu	Asp	Val	His	Ile	Phe	Ile	Arg	Ser	Gln	Lys	Thr	Gly	85	90	95	
Gly	Lys	Gly	Val	Ala	Leu	Glu	Leu	Pro	Lys	Pro	Trp	Glu	Thr	Asp	Lys	100	105	110	
Trp	Leu	Glu	Trp	Ile	Glu	Lys	Arg	Phe	Arg	Glu	Asn	Gly	Leu	Leu	Ile	115	120	125	
Asp	Lys	Asp	Ala	Leu	Gln	Leu	Phe	Phe	Ser	Lys	Val	Gly	Thr	Asn	Asp	130	135	140	
Leu	Ile	Ile	Glu	Arg	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Tyr	Ser	Glu	Asp	145	150	155	160
Arg	Lys	Ile	Thr	Val	Glu	Asp	Val	Glu	Glu	Val	Val	Phe	Thr	Tyr	Gln	165	170	175	
Thr	Pro	Gly	Tyr	Asp	Asp	Phe	Cys	Phe	Ala	Val	Ser	Glu	Gly	Lys	Arg	180	185	190	
Lys	Leu	Ala	His	Ser	Leu	Leu	Ser	Gln	Leu	Trp	Lys	Thr	Thr	Glu	Ser	195	200	205	
Val	Val	Ile	Ala	Thr	Val	Leu	Ala	Asn	His	Phe	Leu	Asp	Leu	Phe	Lys	210	215	220	
Ile	Leu	Val	Leu	Val	Thr	Lys	Lys	Arg	Tyr	Tyr	Thr	Trp	Pro	Asp	Val	225	230	235	240
Ser	Arg	Val	Ser	Lys	Glu	Leu	Gly	Ile	Pro	Val	Pro	Arg	Val	Ala	Arg	245	250	255	
Phe	Leu	Gly	Phe	Ser	Phe	Lys	Thr	Trp	Lys	Phe	Lys	Val	Met	Asn	His	260	265	270	
Leu	Leu	Tyr	Tyr	Asp	Val	Lys	Lys	Val	Arg	Lys	Ile	Leu	Arg	Asp	Leu	275	280	285	
Tyr	Asp	Leu	Asp	Arg	Ala	Val	Lys	Ser	Glu	Glu	Asp	Pro	Lys	Pro	Phe	290	295	300	
Phe	His	Glu	Phe	Ile	Glu	Glu	Val	Ala	Leu	Asp	Val	Tyr	Ser	Leu	Gln	305	310	315	320

Arg Asp Glu Glu

<210> 147
<211> 936
<212> DNA
<213> *Thermatoga maritima*

<400> 147
atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60
gaaaagtctg aaggaatatc catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgttctg 180
gagatagatc ccgaggggga gaacataggc atagacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
atgacccagc aggcggcgaa cgcgtttctg aaggcccttg aagaaccacc agaatacgct 360
gtgatcggtc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaacttggtg cggaaaaact ttctggattg atggaaagtc tcaaagtttt ggagacggaa 600
aaactcttga aaaagggtcct ttcaaaaggc ctcgaagggt atctcgcatg tagggagctc 660
ctggagagat tttcaaagggt ggaatcgaag gaattctttg cgctttttga tcaggtgact 720
aacacgataa caggaaaaga cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
cacgaaaaca catgggaaag cgttgaagat caaaaaagcg tgtctttcct cgattcaatt 840
ctcaggggtg agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936

<210> 148
<211> 311
<212> PRT
<213> *Thermatoga maritima*

<400> 148
Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
1 5 10 15
Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
20 25 30
Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
35 40 45
Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
50 55 60
Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
65 70 75 80

Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His
 85 90 95

Asp Cys Glu Arg Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala
 100 105 110

Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg
 115 120 125

Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val
 130 135 140

Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly
 145 150 155 160

Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala
 165 170 175

Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu
 180 185 190

Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser
 195 200 205

Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe
 210 215 220

Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr
 225 230 235 240

Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr
 245 250 255

Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Lys Ser
 260 265 270

Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu Asn
 275 280 285

Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg Lys
 290 295 300

Arg Gly Val Asn Ala Trp Ser
 305 310

<210> 149

<211> 423
 <212> DNA
 <213> *Thermatoga maritima*

<400> 149
 atgtctttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60
 tacacgctca gcggaactcc agtcaccacc ttcaccatag cgggtggacag gggtcccaga 120
 aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcgtcac ctttggaaga 180
 ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcgt cgaaggtgaa 240
 atgagaatga gaagatggga aacacccact ggagaaaaga gggatatctcc ggaggttggtc 300
 gcaaacgttg ttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
 gagctggaaa taccggaaga agacttttcc agcgatacct tcagtgaaga tgaaccacca 420
 ttt 423

<210> 150
 <211> 141
 <212> PRT
 <213> *Thermatoga maritima*

<400> 150
 Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
 1 5 10 15
 Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr
 20 25 30
 Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
 35 40 45
 Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
 50 55 60
 Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
 65 70 75 80
 Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
 85 90 95
 Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
 100 105 110
 Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp
 115 120 125
 Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
 130 135 140

<210> 151
 <211> 1353
 <212> DNA
 <213> *Thermatoga maritima*

<400> 151
 atgcgtgttc ccccgcacaa cttagaggcc gaagttgctg tgctcggaag catattgata 60
 gatccgtcgg taataaacga cgttcttgaa attttgagcc acgaagattt ctatctgaaa 120
 aaacaccaac acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggac 180
 gtggtttccg tctgtgacaa gcttcaaagc atgggaaaac tcgaggaagt aggtggagat 240
 ctggaagtgg ccagctcgc tgaggctgtg ccagttctg cacacgcact tcactacgcg 300
 gagatcgtca aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
 gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgata 420
 ttcgagatct cagagatgaa aacgacaaaa tcctacgata atctgagagg catcatgcac 480
 cgggtgtttg aaaacctgga gaacttcagg gaaagagcca accttataga acccggtgtg 540
 ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac agggttccac 600
 agctccgata tgggtgataat agcagcgaga ccctccatgg gaaaaacctc cttcgcactc 660
 tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
 atgtccaagg aacagctcgc tcaaagacta ctcagcatgg agtccggtgt ggatctttac 780
 agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggcttct 840
 aaactctaca aagcaccat agttgtggac gatgagtcac tcctcgatcc gcgatcgttg 900
 agggcaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccatttt tgtcgactat 960
 ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagata 1020
 tcgagatctc tgaagctcct tgcgagggaa ctcgacatag tggatgatac gctttcacag 1080
 ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcagggaa 1140
 tccggtgcga tagaacagga cgcagacaca gtcattctca tctacaggga ggaatattac 1200
 aggagcaaaa aatccaaaga ggaaagcaag cttcacgaac ctcacgaagc tgaaatcata 1260
 ataggtaaac agagaaacgg tcccgttgga acgatcactc tgatcttcga cccagaaacg 1320
 gttacgttcc atgaagtcga tgtggtgcat tca 1353

<210> 152
 <211> 451
 <212> PRT
 <213> *Thermatoga maritima*

<400> 152
 Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
 1 5 10 15
 Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
 20 25 30
 Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
 35 40 45
 Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val

50		55		60
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp				
65		70		75 80
Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala				
	85		90	95
Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu				
	100		105	110
Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp				
	115		120	125
Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser				
	130		135	140
Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His				
145		150		155 160
Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile				
	165		170	175
Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu				
	180		185	190
Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala				
	195		200	205
Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg				
	210		215	220
Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu				
225		230		235 240
Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly				
	245		250	255
Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp				
	260		265	270
Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val				
	275		280	285
Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala				
	290		295	300
Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr				

305		310		315		320
Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu						
	325			330		335
Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp						
	340			345		350
Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg						
	355			360		365
Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile						
	370			375		380
Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr						
	385			390		400
Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu						
	405			410		415
Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile						
	420			425		430
Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val						
	435			440		445
Val His Ser						
	450					

<210> 153
 <211> 1695
 <212> DNA
 <213> *Thermatoga maritima*

<400> 153
 gtgattcctc gagaggtcat cgaggaaata aaagaaaagg ttgacatcgt agaggtcatt 60
 tccgagtagc tgaatcttac ccgggtaggt tcctcctaca gggctctctg tccctttcat 120
 tcagaaacca atccttcttt ctacgttcat ccgggtttga agatatacca ttgtttcggc 180
 tgcggtgcga gtggagacgt catcaaattt cttcaagaaa tggaagggat cagtttccag 240
 gaagcgctgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaa 300
 gggacttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtacgtc 360
 aaagagctgg agaaatcgaa agaggcaaaa gactatttaa aaagcagagg cttctctgaa 420
 gaagatatag caaagttcgg ctttgggtac gtccccaaaga gatccagcat ctctatagaa 480
 gttgcagaag gcatgaacat aacactggaa gaacttgtca gatacggat cgcgctgaaa 540
 aagggtgatc gattcgttga tagattcgaa ggaagaatcg ttgttccaat aaagaacgac 600
 agtggtcata ttgtggcttt tgggtggcgt gctctcggca acgaagaacc gaagtatttg 660
 aactctccag agaccaggta tttttcgaag aagaagaccc tttttctctt cgatgaggcg 720

```

aaaaaagtgg caaaagaggt tgggttttttc gtcatcacccg aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaactttc ggcgtattcg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaatcc ctcgaggatc tcctagacta cgaattcaac 960
gtgcttgtgg caacccccctc tccttataaaa gaccagatg aactctttca gaaagaagga 1020
gaagggtcat tgaaaaagat gctgaaaaaac tcgcggttcgt tcgaatattt tctggtgacg 1080
gctggtgagg tcttcttttg caggaacagc cccgcgggtg tgagatccta cctttctttc 1140
ctcaaagggt ggggtccaaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg tttcatcttc tctccagata ccagaaaacc agattttgaa cttttttgaa 1260
agcgacaggc ctaacactat gcctgttcat gagaccaagt cgtcaaaggc ttacgatgag 1320
gggagaggac tggcttattt gtttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaaac gcgagggagt ttttcaagag agtctcactg 1440
ggagaagatt tgaacaaagt catagaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccgaga aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgag aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctcctcaga 1680
aaaataaaga ggagg                                     1695

```

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

```

Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
  1              5              10              15

Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
      20              25              30

Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
      35              40              45

Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
      50              55              60

Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
      65              70              75              80

Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
      85              90              95

Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
      100             105             110

Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
      115             120             125

```

Ala	Lys	Asp	Tyr	Leu	Lys	Ser	Arg	Gly	Phe	Ser	Glu	Glu	Asp	Ile	Ala	130	135	140	
Lys	Phe	Gly	Phe	Gly	Tyr	Val	Pro	Lys	Arg	Ser	Ser	Ile	Ser	Ile	Glu	145	150	155	160
Val	Ala	Glu	Gly	Met	Asn	Ile	Thr	Leu	Glu	Glu	Leu	Val	Arg	Tyr	Gly	165	170	175	
Ile	Ala	Leu	Lys	Lys	Gly	Asp	Arg	Phe	Val	Asp	Arg	Phe	Glu	Gly	Arg	180	185	190	
Ile	Val	Val	Pro	Ile	Lys	Asn	Asp	Ser	Gly	His	Ile	Val	Ala	Phe	Gly	195	200	205	
Gly	Arg	Ala	Leu	Gly	Asn	Glu	Glu	Pro	Lys	Tyr	Leu	Asn	Ser	Pro	Glu	210	215	220	
Thr	Arg	Tyr	Phe	Ser	Lys	Lys	Lys	Thr	Leu	Phe	Leu	Phe	Asp	Glu	Ala	225	230	235	240
Lys	Lys	Val	Ala	Lys	Glu	Val	Gly	Phe	Phe	Val	Ile	Thr	Glu	Gly	Tyr	245	250	255	
Phe	Asp	Ala	Leu	Ala	Phe	Arg	Lys	Asp	Gly	Ile	Pro	Thr	Ala	Val	Ala	260	265	270	
Val	Leu	Gly	Ala	Ser	Leu	Ser	Arg	Glu	Ala	Ile	Leu	Lys	Leu	Ser	Ala	275	280	285	
Tyr	Ser	Lys	Asn	Val	Ile	Leu	Cys	Phe	Asp	Asn	Asp	Lys	Ala	Gly	Phe	290	295	300	
Arg	Ala	Thr	Leu	Lys	Ser	Leu	Glu	Asp	Leu	Leu	Asp	Tyr	Glu	Phe	Asn	305	310	315	320
Val	Leu	Val	Ala	Thr	Pro	Ser	Pro	Tyr	Lys	Asp	Pro	Asp	Glu	Leu	Phe	325	330	335	
Gln	Lys	Glu	Gly	Glu	Gly	Ser	Leu	Lys	Lys	Met	Leu	Lys	Asn	Ser	Arg	340	345	350	
Ser	Phe	Glu	Tyr	Phe	Leu	Val	Thr	Ala	Gly	Glu	Val	Phe	Phe	Asp	Arg	355	360	365	
Asn	Ser	Pro	Ala	Gly	Val	Arg	Ser	Tyr	Leu	Ser	Phe	Leu	Lys	Gly	Trp	370	375	380	

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400

Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415

Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430

Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445

Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460

Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480

Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495

Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510

Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525

Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540

Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560

Lys Ile Lys Arg Arg
 565

<210> 155
 <211> 804
 <212> DNA
 <213> Thermus thermophilus

<400> 155
 atggctctac acccggtca ccctggggca ataatcgggc acgaggccgt tctcgccctc 60
 cttccccgcc tcaccgcca gaccctgctc ttctccggcc ccgagggggt ggggcggcgc 120
 accgtggccc gctggtaacgc ctgggggctc aaccgcggct tcccccgcc ctccctgggg 180
 gagcaccgg acgtcctcga ggtggggccc aaggcccgga acctccgggg ccgggcccag 240

```

gtgCGGctgg aggaggtggc gcccctcttg gagtggtgct ccagccaccc ccgggagcgg 300
gtgaaggtgg ccatcctgga ctCGGcccaC ctctcaccg aggcCGccgc caacGCCctc 360
ctcaagctcc tggaggagcc cccttcctac gcccgcacgc tcctcatcgc cccaagccgc 420
gccaccctcc tccccaccct ggCctcccgG gccacggagg tggcattcgc ccccgTgccc 480
gaggaggccc tgcgcgcCct caccCaggac ccggagctcc tccgctacgc cgcCGgggccc 540
ccgggcccgc tccttagggc cctccaggac ccggaggggt accgggcccG catggccagg 600
gcgcaaaggG tcctgaaagc ccCGccCctg gagcgcctcG ctttgcttcG ggagcttttg 660
gccgaggagg aggggggtcca cgcCctccac gccgtcctaA agcgcCcgga gcacctcctt 720
gccctggagc gggcgcggga ggCctggag gggTacgtga gcccCgagct ggtCctcgcc 780
cggctggcct tagacttaga gaca                                     804

```

```

<210> 156
<211> 268
<212> PRT
<213> Thermus thermophilus

```

```

<400> 156
Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
  1                      5              10              15

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
      20              25              30

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
      35              40              45

Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp
      50              55              60

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
      65              70              75              80

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
      85              90              95

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
      100             105             110

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
      115             120             125

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
      130             135             140

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
      145             150             155             160

```

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
 165 170 175
 Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu
 180 185 190
 Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro
 195 200 205
 Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu
 210 215 220
 Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu
 225 230 235 240
 Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu
 245 250 255
 Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr
 260 265

<210> 157
 <211> 729
 <212> DNA
 <213> Thermus thermophilus

<400> 157
 atgctggacc tgagggaggt gggggaggcg gagtggaagg ccctaaagcc ccttttggaa 60
 agcgtgcccc agggcgctccc cgctcctcctc ctggacccta agccaagccc ctcccgggcg 120
 gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180
 cggcacctgg aaaaccgggc caagcgcttg gggctcaggc tcccgggcg ggtggcccag 240
 tacctggcct ccctggaggg ggacctcgag gccctggagc gggagctgga gaagcttgcc 300
 ctctctctccc caccctcac cctggagaag gtggagaagg tgggtggccct gaggcccccc 360
 ctcacgggct ttgacctggt gcgctccgtc ctggagaagg accccaagga ggccctcctg 420
 cgcctaggcg gcctcaagga ggagggggag gagccctca ggctcctcgg ggccctctcc 480
 tggcagttcg ccctcctcgc ccgggccttc ttctcctcc gggaaaaccc caggcccaag 540
 gaggaggacc tcgcccgcct cgaggccac ccctacgccg ccgcccgcgc cctggaggcg 600
 gcgaagcgcc tcacggaaga ggccctcaag gaggccttg acgccctcat ggaggcggaa 660
 aagagggcca agggggggaa agaccctggt ctgcctctgg aggcggcggt cctccgcctc 720
 gcccgttga 729

<210> 158
 <211> 292
 <212> PRT
 <213> Thermus thermophilus

<400> 158

Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
50 55 60

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
65 70 75 80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
85 90 95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
100 105 110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
115 120 125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
130 135 140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
145 150 155 160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
165 170 175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
180 185 190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
195 200 205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
210 215 220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
225 230 235 240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
245 250 255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275 280 285

Arg Leu Ala Arg
290

<210> 159
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159
gtgtgtcata tgagtaagga tttcgtccac cttcacc 37

<210> 160
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gtgtgtggat ccggggacta ctcggaagta aggg 34

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gtgtgtcata tggaaccac aatattccag ttccag 36

<210> 162

<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 162
gtgtgtggat ccttatccac catgagaagt atttttcac 39

<210> 163
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 163
gtgtgtcata tggaaaaagt tttttttgga aaaaactcca g 41

<210> 164
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 164
gtgtgtggat ccttaatccg cctgaacggc taacg 35

<210> 165
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 165
gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g 41

<210> 166

<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 166
gtgtgtggat ccttaaaaca gcctcgtccc gctgga 36

<210> 167
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 167
gtgtgtcata tgcgcgttaa ggtggacagg gag 33

<210> 168
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 168
tgtgtctcga gtcattgcta caccctcatc ggcatt 35

<210> 169
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 169
gtgtgtcata tgctcaataa ggtttttata ataggaagac ttacggg 47

<210> 170

<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gtgtggatcc ttaaaaaggt atttcgtcct cttcatcgg 39

<210> 171
<211> 807
<212> DNA
<213> Thermus thermophilus

<400> 171
atggctcgag gcctgaaccg cgttttcctc atcggcgccc tcgccacccg gccggacatg 60
cgctacaccc cggcgggggt cgccattttg gacctgacce tcgccgggtca ggacctgctt 120
ctttccgata acggggggga accggagggtg tcctggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgacctcttg gaccaagggc agctcgtctt cgtggagggc 240
cgcctggagt accgccagtg ggaaagggag ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggaccccctg gacgaccggg ggaagaagcg ggcggaggac agccggggcc 360
agcccaggct ccgcgccgcc ctgaaccagg tcttcctcat gggcaacctg acccggggacc 420
cggaactccg ctacaccccc cagggcaccc cggtggcccc gctgggcctg gcggtgaacg 480
agcgccgcca gggggcgagg gagcgacccc acttcgtgga ggttcaggcc tggcgcgacc 540
tggcggagtg ggccgccgag ctgaggaagg gcgacggcct tttcgtgate ggcaggttgg 600
tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccctg gtggaggccc 660
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720
cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccgccgg 780
aggaggattt gccgttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> Thermus thermophilus

<400> 172
Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15
Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30
Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45

<400> 173

```
aattccgaca tttcaattga atcgttttatt ccgcttgaaa aagaaggcaa gttgctcggt 60
gatgtgaaaa gaccggggag catcgctactg caggcgcgct ttttctctga aatcgtgaaa 120
aaactgccgc aacaaacggt ggaaatcgaa acggaagaca actttttgac gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaacgccg acgaatatcc gcgcctgccg 240
caaattgaag aagaaaacgt gtttcaaadc ccggctgatt tattgaaaac cgtgattcgg 300
caaacgggtgt tcgccgtttc tacatcggaa acgcgcccaa tcttgacagg tgtcaactgg 360
aaagttgaac atggcgagct tgtctgcaca gcgaccgaca gtcacgcctt agccatgcgc 420
aaagtgaana ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaagt 480
cttaatgagc tcagcaaaat tttggatgac ggcaaccacc cgggtggacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttctcttct tttcccggt gcttgacggc 600
aactatccgg agacggcccg cttgattcca acagaaagca aaacgaccat gatcgtcaat 660
gcaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaa 720
aacgttgtga aactgacgac gcttcttggg ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cgttgcgggc gcttgatgga acagacattt 900
caaatcagct tcaactggggc catgcggccg ttcctgttgc gcccgcttca accgattcga 960
tgcttcagct cattttgccg gtgagaacat at 992
```

<210> 174

<211> 334

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 174

```
Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
 1             5             10             15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
20             25             30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
35             40             45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
50             55             60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
65             70             75             80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
85             90             95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
100            105            110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
```

115		120		125
Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys				
130		135		140
Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly				
145		150		155
				160
Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His				
		165		170
				175
Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu				
		180		185
				190
His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr				
		195		200
				205
Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala				
		210		215
				220
Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu				
225		230		235
				240
Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu				
		245		250
				255
Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu				
		260		265
				270
Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala				
		275		280
				285
Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln				
		290		295
				300
Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His				
305		310		315
				320
Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr				
		325		330

<210> 175

<211> 492

<212> DNA

<213> Bacillus stearothermophilus

<400> 175

```

atgattaacc gcgtcatttt ggtcggcagg ttaacgagag atccggagtt gcgttacact 60
ccaagcggag tggctgttgc cacgtttacg ctgcgcgtca accgtccgtt tacaaatcag 120
cagggcgagc gggaaacgga ttttattcaa tgtgtcgttt ggccgcccca ggcggaaaac 180
gtcgccaact ttttgaaaaa ggggagcttg gctggtgtcg atggccgact gcaaaccgc 240
agctatgaaa atcaagaagg tcggcgtgtg tacgtgacgg aagtgggtggc tgatagcgtc 300
caatttcttg agccgaaagg aacgagcgag cagcgagggg cgacagcagg cggctactat 360
ggggatccat tcccatcgg gcaagatcag aaccaccaat atccgaacga aaaagggttt 420
ggccgcacgc atgacgatcc ttctcgccaat gacggccagc cgatcgatat ttctgatgat 480
gatttgccgt tt 492

```

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

```

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
  1             5             10             15

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
      20             25             30

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
      35             40             45

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
      50             55             60

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
      65             70             75             80

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
      85             90             95

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
      100            105            110

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
      115            120            125

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
      130            135            140

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
      145            150            155            160

Asp Leu Pro Phe

```

<210> 177
 <211> 1044
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 177
 atgctggaac gcgtatgggg aaacattgaa aaacggcggt tttctcccct ttatttatta 60
 tacggcaatg agccgttttt attaacggaa acgtatgagc gattggtgaa cgcagcgctt 120
 ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaaac gccgatcgag 180
 gcggcgcttg aggaggccga gacgggtgccg tttttcggcg agcggcggtg cattctcatc 240
 aagcatccat attttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
 ctggaggcgt acttgaaggc gccgtcgccg ttttcgatcg tcgtcttttt cgcgccgtac 360
 gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaag cgaagtcgtc 420
 atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480
 caaggggagc aagcaagcga cgaggcgatt gatgtcctgt tgcggcgggc cgggacgcag 540
 ctttccgcct tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600
 atcgaggcgg cggcggttga gcggcttgtc gcccgcacgc cggaagaaaa cgtatttgtg 660
 cttgtcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720
 cttgaaaaca atgaagagcc gatcaaaatt ttggcggttg tcgccgccca tttccgcttg 780
 ctttcgcaag tgaaatggct tgcctcctta ggctacggac aggcgcaaat tgctgcggcg 840
 ctcaaggtgc acccgttccg cgtcaagctc gctcttgctc aagcggcccg cttecgctgac 900
 ggagagcttg ctgaggcgat caacgagctc gctgacgccg attacgaagt gaaaagcggg 960
 gcggtcgatc gccggttggc cgttgagctg cttctgatgc gctggggcgc ccgcccggcg 1020
 caagcggggc gccacggccg gcgg 1044

<210> 178
 <211> 348
 <212> PRT
 <213> *Bacillus stearothermophilus*

<400> 178
 Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
 1 5 10 15
 Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
 20 25 30
 Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
 35 40 45
 Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
 50 55 60
 Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
 . 340 345

<210> 179

<211> 757

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 179

```

atgcatggg aacagctagc gaaacgccag ccggtggtgg cgaaaatgct gcaaagcggc 60
ttggaaaaag ggcggatttc tcatgcgtac ttgtttgagg ggcagcgggg gacgggcaaa 120
aaagcggcca gtttggtggt ggcgaaacgt ttgttttgtc tgtccccaat cggagtttcc 180
ccgtgtctag agtgccgcaa ctgccggcgc atcgactccg gcaaccaccc tgacgtccgg 240
gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300
ttctcgaaaa cagcggtcga gtcggataaa aaaatgtaca tcgttgagca cgccgatcaa 360
atgacgacaa gcgctgccaa cagccttctg aaatTTTTTgg aagagccgca tccgggggacg 420
gtggcggtat tgctgactga gcaataccac cgctgctag ggacgatcgt ttcccgtgt 480
caagtgcctt cgttccggcc gttgccggcc gcagagctcg cccagggact tgtcgaggag 540
cacgtgccgt tgccgttggc gctgttggct gcccatTTTga caaacagctt cgaggaagca 600
ctggcgcttg ccaaagatag ttggtttgcc gaggcgcgaa cattagtgt acaatggtat 660
gagatgctgg gcaagccgga gctgcagctt ttgtttttca tccacgaccg cttgttttccg 720
catttttttg aaagccatca gcttgacctt ggacttg 757

```

<210> 180

<211> 252

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 180

```

Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
  1           5           10           15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
      20           25           30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
      35           40           45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
      50           55           60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
      65           70           75           80

```

Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp
 85 90 95
 Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met
 100 105 110
 Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser
 115 120 125
 Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu
 130 135 140
 Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys
 145 150 155 160
 Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly
 165 170 175
 Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His
 180 185 190
 Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp
 195 200 205
 Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly
 210 215 220
 Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro
 225 230 235 240
 His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu
 245 250

<210> 181

<211> 1677

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 181

gtggcatacc aagcggttata tcgcgtgttt cggccgcagc gctttgcgga catggtcggc 60
 caagaacacg tgaccaagac gttgcaaagc gccctgcttc aacataaaat atcgcacgct 120
 tacttatttt ccggcccgcg cggtagagga aaaacgagcg cagcgaaaat tttcgccaag 180
 gcggtcaact gtgaacaggc gccagcggcg gagccatgca atgagtgtcc agcttgccctc 240
 ggcattacga atggaacggt tcccgatgtg ctggaaattg acgctgcttc caacaaccgc 300
 gtcgatgaaa ttcgtgatat ccgtgagaag gtgaaatttg cgccaacgtc ggcccgcctac 360
 aaagtgtata tcatcgacga ggtgcatatg ctgtcgatcg gtgcgtttta cgcgctgttg 420
 aaaacggttg aggagccgcc gaaacacgtc attttcattt tggccacgac cgagccgcac 480


```

aaaattccgg cgacgatcat ttcccgtgc caacgggttcg attttcgccg catcccgtt 540
caggcgatcg ttacacggct aaagtacgtc gcaagcgccc aagggtgtcga ggcgtcagat 600
gaggcattgt ccgccatcgc ccgtgctgca gacgggggga tgcgcgatgc gctcagcttg 660
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg catcatttgc cgccttatcg agcttcacgc aagccatcca ccgcaaagat 780
acagcggcgg ttcttcagca cttggaaacg atgatggcgc aagggaaga tccgcatcgt 840
ttggttgaag acttgatatt gtactatcgc gatttattgc tgtacaaaac cgctccctat 900
gtggaggagg cgattcaaat tgctgtcgtt gacgaagcgt tcacttcact gtcggaaatg 960
attccgggtt ccaatttata cgaggccatc gagttgctga acaaaagcca gcaagagatg 1020
aagtggacaa accacccgcg ctttctgttg gaagtggcgc ttgtgaaact ttgccatcca 1080
tcagccgccg ccccgtcgct gtcggcttcc gagttggaac cgttgataaa gcggattgaa 1140
acgctggagg cggaattgcg gcgcctgaag gaacaaccgc ctgcccctcc gtcgaccgcc 1200
gcgccggtga aaaaactgtc caaacccgatg aaaacggggg gatataaagc cccggttggc 1260
cgcatttacg agctgttgaa acaggcgacg catgaagatt tagctttggt gaaaggatgc 1320
tgggcggatg tgctcgacac gttgaaacgg cagcataaag tgctgcacgc tgccttgctg 1380
caagagagcg agccggttgc agcgagcgcc tcagcgtttg tattaataatt caaatagaa 1440
atccactgca aaatggcgac cgatcccaca agttcgggtc aagaaaacgt cgaagcgatt 1500
ttgtttgagc tgacaaaccg ccgctttgaa atggttagcca ttccggaggg agaatgggga 1560
aaaataagag aagagttcat ccgcaataag gacgccatgg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggctgttt ggcaagagc tgatcgaaat taaagaa 1677

```

<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

```

Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
 1              5              10              15

Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
      20              25              30

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
      35              40              45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
 50              55              60

Glu Gln Ala Pro Ala Ala Glu Pro Cys Asn Glu Cys Pro Ala Cys Leu
65              70              75              80

Gly Ile Thr Asn Gly Thr Val Pro Asp Val Leu Glu Ile Asp Ala Ala
      85              90              95

Ser Asn Asn Arg Val Asp Glu Ile Arg Asp Ile Arg Glu Lys Val Lys
100              105              110

```

Phe	Ala	Pro	Thr	Ser	Ala	Arg	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	115	120	125
His	Met	Leu	Ser	Ile	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	130	135	140
Glu	Pro	Pro	Lys	His	Val	Ile	Phe	Ile	Leu	Ala	Thr	Thr	Glu	Pro	His	145	150	155
Lys	Ile	Pro	Ala	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Arg	Phe	Asp	Phe	Arg	165	170	175
Arg	Ile	Pro	Leu	Gln	Ala	Ile	Val	Ser	Arg	Leu	Lys	Tyr	Val	Ala	Ser	180	185	190
Ala	Gln	Gly	Val	Glu	Ala	Ser	Asp	Glu	Ala	Leu	Ser	Ala	Ile	Ala	Arg	195	200	205
Ala	Ala	Asp	Gly	Gly	Met	Arg	Asp	Ala	Leu	Ser	Leu	Leu	Asp	Gln	Ala	210	215	220
Ile	Ser	Phe	Ser	Asp	Gly	Lys	Leu	Arg	Leu	Asp	Asp	Val	Leu	Ala	Met	225	230	235
Thr	Gly	Ala	Ala	Ser	Phe	Ala	Ala	Leu	Ser	Ser	Phe	Ile	Glu	Ala	Ile	245	250	255
His	Arg	Lys	Asp	Thr	Ala	Ala	Val	Leu	Gln	His	Leu	Glu	Thr	Met	Met	260	265	270
Ala	Gln	Gly	Lys	Asp	Pro	His	Arg	Leu	Val	Glu	Asp	Leu	Ile	Leu	Tyr	275	280	285
Tyr	Arg	Asp	Leu	Leu	Leu	Tyr	Lys	Thr	Ala	Pro	Tyr	Val	Glu	Gly	Ala	290	295	300
Ile	Gln	Ile	Ala	Val	Val	Asp	Glu	Ala	Phe	Thr	Ser	Leu	Ser	Glu	Met	305	310	315
Ile	Pro	Val	Ser	Asn	Leu	Tyr	Glu	Ala	Ile	Glu	Leu	Leu	Asn	Lys	Ser	325	330	335
Gln	Gln	Glu	Met	Lys	Trp	Thr	Asn	His	Pro	Arg	Leu	Leu	Leu	Glu	Val	340	345	350
Ala	Leu	Val	Lys	Leu	Cys	His	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Ser	355	360	365

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380
 Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400
 Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415
 Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430
 Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445
 Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460
 Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480
 Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495
 Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510
 Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525
 Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540
 Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183
 <211> 4301
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 183
 atggtgacaa aagagcaaaa agagcggttt ctcatcctgc ttgagcagct gaagatgacg 60
 tcggacgaat ggatgccgca ttttcgtgag gcagccattc gcaaagtcgt gatcgataaa 120
 gaggagaaaa gctggcattt ttattttcag ttcgacaacg tgctgccggt tcatgtatac 180
 aaaacgtttg ccgatcggct gcagacggcg ttccgccata tcgccgccgt ccgccatac 240

atggagggtcg	aagcgccgcg	cgtaactgag	gcggatgtgc	aggcgtattg	gccgctttgc	300
cttgccgagc	tgcaagaagg	catgtcgccg	cttggtcgatt	ggctcagccg	gcagacgcct	360
gagctgaaag	gaaacaagct	gcttggtcgtt	gcccgcctatg	aagcggaagc	gctggcgatc	420
aaacggcggt	tcgccaaaaa	aatcgctgat	gtgtacgctt	cgtttgggtt	tccccccctt	480
cagcttgacg	tcagcgtcga	gccgtccaag	caagaaatgg	aacagttttt	ggcgcaaaaa	540
cagcaagagg	acgaagagcg	agcgcttgct	gtactgaccg	atttagcgag	ggaagaagaa	600
aaggccgcgt	ctgcgccgcc	gtccggtccg	cttggtcatcg	gctatccgat	ccgcgacgag	660
gagccggtgc	ggcggttga	aacgatcgtc	gaagaagagc	ggcgcgtcgt	tgtgcaaggc	720
tatgtatttg	acgccgaagt	gagcgaatta	aaaagcggcc	gcacgctgtt	gaccatgaaa	780
atcacagatt	acacgaactc	gatttttagtc	aaaatgttct	cgcgcgacaa	agaggacgcc	840
gagcttatga	gcggcgtcaa	aaaaggcatg	tgggtgaaag	tgcgcggcag	cgtgcaaaac	900
gatacgttcg	tccgtgattt	gggtcatcatc	gccaacgatt	tgaacgaaat	cgccgcaaac	960
gaacggcaag	atacggcgcc	ggaaggggaa	aagaggggtcg	agctccattt	gcataccccg	1020
atgagccaaa	tggacgcggt	cacctcggtg	acaaaactca	ttgagcaagc	gaaaaaatgg	1080
gggcatccgg	cgatcgccgt	caccgaccat	gccgttggtc	agtcgtttcc	ggaggcctac	1140
agcgcggcga	aaaaacacgg	catgaaggtc	atttacggcc	ttgaggcgaa	catcgtcgac	1200
gatggcggtgc	cgatcgccct	caatgagacg	caccgcccgtc	tttcggagga	aacgtacgtc	1260
gtctttgacg	tcgagacgac	gggcctgtcg	gctgtgtaca	atacgatcat	tgagctggcg	1320
gcggtgaaag	tgaaagacgg	cgagatcatc	gaccgattca	tgtcgtttgc	caaccctgga	1380
catccgttgt	cggtgacaac	gatggagctg	actgggatca	ccgatgagat	ggtgaaagac	1440
gccccgaagc	cggacgaggt	gctagcccgt	tttgttgact	gggcccgcga	tgcgacgctt	1500
gttgcccaca	acgccagctt	tgacatcggt	tttttaaacg	cgggcctcgc	tcgcatgggg	1560
cgcggcacaaa	tcgcgaatcc	agtcatcgat	acgctcgagc	tggcccgttt	tttatacccc	1620
gatttgaaaa	accatcggtc	caatacattg	tgcaaaaaat	ttgacattga	attgacgcag	1680
catcacccgcg	ccatctacga	cgcgaggcg	accgggcatt	tgcttatgcg	gctgttgaag	1740
gaagcggaag	agcgcgccat	actgtttcat	gacgaattaa	acagccgcac	gcacagcgaa	1800
gcgtccctatc	ggcttgcgcg	cccgttccat	gtgacgctgt	tggcgcaaaa	cgagactgga	1860
ttgaaaaatt	tgttcaagct	tgtgtcattg	tcgcacattc	aatattttca	ccgtgtgccg	1920
cgcatcccgc	gctccgtgct	cgtcaagcac	cgcgacggcc	tgcttgctcg	ctcgggctgc	1980
gacaaaggag	agctgtttga	caacttgatc	caaaaggcgc	cggaagaagt	cgaagacatc	2040
gcccgttttt	acgattttct	tgaagtgcac	ccgccggacg	tgtacaagcc	gctcatcgag	2100
atggattatg	tgaaagacga	agagatgatc	aaaaacatca	tccgcagcat	cgtcgccctt	2160
ggtgagaagc	ttgacatccc	ggttggtcgcc	actggcaacg	tccattactt	gaaccagaa	2220
gataaaattt	accggaaaat	cttaatccat	tcgcaaggcg	gggcgaatcc	gctcaaccgc	2280
catgaactgc	cggatgtata	tttccgtacg	acgaatgaaa	tgcttgactg	cttctcgttt	2340
ttagggcccg	aaaaagcgaa	ggaaatcgtc	gttgacaaca	cgcaaaaaat	cgcttcgtta	2400
atcggcgatg	tcaagccgat	caaagatgag	ctgtatacgc	cgcgcatatga	aggggcggac	2460
gaggaaatca	gggaaatgag	ctaccggcg	gcgaaggaaa	tttacggcga	cccgttgccg	2520
aaacttgttg	aagagcggct	tgagaaggag	ctaaaaagca	tcatcggccca	tggctttgcc	2580
gtcattttatt	tgatctcgca	caagcttggtg	aaaaaatcgc	tcgatgacgg	ctaccttgtc	2640
gggtcgcgcg	gatcggtcgg	ctcgtcgttt	gtcgcgacga	tgacggaaat	caccgaggtc	2700
aatccgctgc	cgccgcatta	cgtttgcccc	aactgcaagc	attcgaggtt	ctttaacgac	2760
ggttcagtcg	gctcagggtt	tgatttgccg	gataaaaact	gcccgcgatg	tgggacgaaa	2820
tacaagaaag	acgggcacga	catcccgttt	gagacgtttc	tcggctttta	aggcgacaaa	2880
gtgccggata	tcgacttgaa	cttttccggc	gaataaccagc	cgcgcgccca	caactatacg	2940
aaagtgctgt	ttggcgaaga	caacgtctac	cgcgccggga	cgattggcac	ggtcgctgac	3000
aaaacggcgt	acggatttgt	caaagcgtat	gcgagcgacc	ataacttaga	gctgcgcggc	3060
gcggaaatcg	acggctcgcg	gctggctgca	ccgggggtgaa	gcggacgacc	gggcagcatc	3120

```

cgggcgccat catcgctcgc ccggattata tggaaattta cgatttttacg ccgattcaat 3180
atccggccga tgacacgtcc tctgaatggc ggacgaccca ttctgacttc cattcgatcc 3240
acgacaattt gttgaagctc gatattctcg ggcacgacga tccgacggtc attcgcatgc 3300
tgcaagattt aagcggcatc gatccgaaaa cgatcccgac cgacgacccg gatgtgatgg 3360
gcatttttcag cagcaccgag ccgcttggcg ttacgcccga gcaaatcatg tgcaatgtcg 3420
gcacgatcgg cattccggag tttggcacgc gcttcgttcg gcaaatggtg gaagagacaa 3480
ggccaaaaac gttttccgaa ctctgtgcaa tttccggcct gtcgcacggc accgatgtgt 3540
ggctcggcaa cgcgcaagag ctcatcmeta acggcacgtg tacgttatcg gaagtcacgc 3600
gctgcccgca cgacattatg gtctatttga tttaccgcgg gctcgagccg tcgctcgctt 3660
ttaaaatcat ggaatccgtg cgcaaaggaa aaggcttaac gccggagttt gaagcagaaa 3720
tgcgcaaaca tgacgtgccg gagtggtaca tcgattcatg caaaaaaatc aagtacatgt 3780
tcccgaagc gcacgccgcc gcctacgtgt taatggcggg gcgcatcgcc tactttaagg 3840
tgcaccatcc gcttttgtat tacgcgtcgt actttacggg gcgggaggag gactttgacc 3900
ttgacgccat gatcaaagga tcacccgcca ttcgcaagcg gattgaggaa atcaacgcca 3960
aaggcattca ggcgacggcg aaagaaaaaa gcttgctcac ggttcttgag gtggccttag 4020
agatgtgcga gcgcggcctt tcctttaaaa atatcgattt gtaccgctcg caggcgacgg 4080
aattcgatc tgacggcaat tctctcatc cgccgttcaa cgccattccg gggcttggga 4140
cgaacgtggc gcaggcgatc gtgcgcgccc gcgaggaagg cgagtttttg tcgaaggagg 4200
atttgcaaca gcgcggcaaa ttgtcgaaaa cgctgctcga gtatctagaa agccgcggct 4260
gccttgactc gcttccagac cataaccagc tgctcgctgtt t 4301

```

<210> 184
 <211> 1433
 <212> PRT
 <213> *Bacillus stearothermophilus*

```

<400> 184
Met Val Thr Lys Glu Gln Lys Glu Arg Phe Leu Ile Leu Leu Glu Gln
  1              5              10              15

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
      20              25              30

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
      35              40              45

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
      50              55              60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
      65              70              75              80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
      85              90              95

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
      100             105             110

```

Asp	Trp	Leu	Ser	Arg	Gln	Thr	Pro	Glu	Leu	Lys	Gly	Asn	Lys	Leu	Leu	115	120	125	
Val	Val	Ala	Arg	His	Glu	Ala	Glu	Ala	Leu	Ala	Ile	Lys	Arg	Arg	Phe	130	135	140	
Ala	Lys	Lys	Ile	Ala	Asp	Val	Tyr	Ala	Ser	Phe	Gly	Phe	Pro	Pro	Leu	145	150	155	160
Gln	Leu	Asp	Val	Ser	Val	Glu	Pro	Ser	Lys	Gln	Glu	Met	Glu	Gln	Phe	165	170	175	
Leu	Ala	Gln	Lys	Gln	Gln	Glu	Asp	Glu	Glu	Arg	Ala	Leu	Ala	Val	Leu	180	185	190	
Thr	Asp	Leu	Ala	Arg	Glu	Glu	Glu	Lys	Ala	Ala	Ser	Ala	Pro	Pro	Ser	195	200	205	
Gly	Pro	Leu	Val	Ile	Gly	Tyr	Pro	Ile	Arg	Asp	Glu	Glu	Pro	Val	Arg	210	215	220	
Arg	Leu	Glu	Thr	Ile	Val	Glu	Glu	Glu	Arg	Arg	Val	Val	Val	Gln	Gly	225	230	235	240
Tyr	Val	Phe	Asp	Ala	Glu	Val	Ser	Glu	Leu	Lys	Ser	Gly	Arg	Thr	Leu	245	250	255	
Leu	Thr	Met	Lys	Ile	Thr	Asp	Tyr	Thr	Asn	Ser	Ile	Leu	Val	Lys	Met	260	265	270	
Phe	Ser	Arg	Asp	Lys	Glu	Asp	Ala	Glu	Leu	Met	Ser	Gly	Val	Lys	Lys	275	280	285	
Gly	Met	Trp	Val	Lys	Val	Arg	Gly	Ser	Val	Gln	Asn	Asp	Thr	Phe	Val	290	295	300	
Arg	Asp	Leu	Val	Ile	Ile	Ala	Asn	Asp	Leu	Asn	Glu	Ile	Ala	Ala	Asn	305	310	315	320
Glu	Arg	Gln	Asp	Thr	Ala	Pro	Glu	Gly	Glu	Lys	Arg	Val	Glu	Leu	His	325	330	335	
Leu	His	Thr	Pro	Met	Ser	Gln	Met	Asp	Ala	Val	Thr	Ser	Val	Thr	Lys	340	345	350	
Leu	Ile	Glu	Gln	Ala	Lys	Lys	Trp	Gly	His	Pro	Ala	Ile	Ala	Val	Thr	355	360	365	

Asp	His	Ala	Val	Val	Gln	Ser	Phe	Pro	Glu	Ala	Tyr	Ser	Ala	Ala	Lys	370	375	380	
Lys	His	Gly	Met	Lys	Val	Ile	Tyr	Gly	Leu	Glu	Ala	Asn	Ile	Val	Asp	385	390	395	400
Asp	Gly	Val	Pro	Ile	Ala	Tyr	Asn	Glu	Thr	His	Arg	Arg	Leu	Ser	Glu	405	410	415	
Glu	Thr	Tyr	Val	Val	Phe	Asp	Val	Glu	Thr	Thr	Gly	Leu	Ser	Ala	Val	420	425	430	
Tyr	Asn	Thr	Ile	Ile	Glu	Leu	Ala	Ala	Val	Lys	Val	Lys	Asp	Gly	Glu	435	440	445	
Ile	Ile	Asp	Arg	Phe	Met	Ser	Phe	Ala	Asn	Pro	Gly	His	Pro	Leu	Ser	450	455	460	
Val	Thr	Thr	Met	Glu	Leu	Thr	Gly	Ile	Thr	Asp	Glu	Met	Val	Lys	Asp	465	470	475	480
Ala	Pro	Lys	Pro	Asp	Glu	Val	Leu	Ala	Arg	Phe	Val	Asp	Trp	Ala	Gly	485	490	495	
Asp	Ala	Thr	Leu	Val	Ala	His	Asn	Ala	Ser	Phe	Asp	Ile	Gly	Phe	Leu	500	505	510	
Asn	Ala	Gly	Leu	Ala	Arg	Met	Gly	Arg	Gly	Lys	Ile	Ala	Asn	Pro	Val	515	520	525	
Ile	Asp	Thr	Leu	Glu	Leu	Ala	Arg	Phe	Leu	Tyr	Pro	Asp	Leu	Lys	Asn	530	535	540	
His	Arg	Leu	Asn	Thr	Leu	Cys	Lys	Lys	Phe	Asp	Ile	Glu	Leu	Thr	Gln	545	550	555	560
His	His	Arg	Ala	Ile	Tyr	Asp	Ala	Glu	Ala	Thr	Gly	His	Leu	Leu	Met	565	570	575	
Arg	Leu	Leu	Lys	Glu	Ala	Glu	Glu	Arg	Gly	Ile	Leu	Phe	His	Asp	Glu	580	585	590	
Leu	Asn	Ser	Arg	Thr	His	Ser	Glu	Ala	Ser	Tyr	Arg	Leu	Ala	Arg	Pro	595	600	605	
Phe	His	Val	Thr	Leu	Leu	Ala	Gln	Asn	Glu	Thr	Gly	Leu	Lys	Asn	Leu	610	615	620	

Phe	Lys	Leu	Val	Ser	Leu	Ser	His	Ile	Gln	Tyr	Phe	His	Arg	Val	Pro	625	630	635	640
Arg	Ile	Pro	Arg	Ser	Val	Leu	Val	Lys	His	Arg	Asp	Gly	Leu	Leu	Val	645	650	655	
Gly	Ser	Gly	Cys	Asp	Lys	Gly	Glu	Leu	Phe	Asp	Asn	Leu	Ile	Gln	Lys	660	665	670	
Ala	Pro	Glu	Glu	Val	Glu	Asp	Ile	Ala	Arg	Phe	Tyr	Asp	Phe	Leu	Glu	675	680	685	
Val	His	Pro	Pro	Asp	Val	Tyr	Lys	Pro	Leu	Ile	Glu	Met	Asp	Tyr	Val	690	695	700	
Lys	Asp	Glu	Glu	Met	Ile	Lys	Asn	Ile	Ile	Arg	Ser	Ile	Val	Ala	Leu	705	710	715	720
Gly	Glu	Lys	Leu	Asp	Ile	Pro	Val	Val	Ala	Thr	Gly	Asn	Val	His	Tyr	725	730	735	
Leu	Asn	Pro	Glu	Asp	Lys	Ile	Tyr	Arg	Lys	Ile	Leu	Ile	His	Ser	Gln	740	745	750	
Gly	Gly	Ala	Asn	Pro	Leu	Asn	Arg	His	Glu	Leu	Pro	Asp	Val	Tyr	Phe	755	760	765	
Arg	Thr	Thr	Asn	Glu	Met	Leu	Asp	Cys	Phe	Ser	Phe	Leu	Gly	Pro	Glu	770	775	780	
Lys	Ala	Lys	Glu	Ile	Val	Val	Asp	Asn	Thr	Gln	Lys	Ile	Ala	Ser	Leu	785	790	795	800
Ile	Gly	Asp	Val	Lys	Pro	Ile	Lys	Asp	Glu	Leu	Tyr	Thr	Pro	Arg	Ile	805	810	815	
Glu	Gly	Ala	Asp	Glu	Glu	Ile	Arg	Glu	Met	Ser	Tyr	Arg	Arg	Ala	Lys	820	825	830	
Glu	Ile	Tyr	Gly	Asp	Pro	Leu	Pro	Lys	Leu	Val	Glu	Glu	Arg	Leu	Glu	835	840	845	
Lys	Glu	Leu	Lys	Ser	Ile	Ile	Gly	His	Gly	Phe	Ala	Val	Ile	Tyr	Leu	850	855	860	
Ile	Ser	His	Lys	Leu	Val	Lys	Lys	Ser	Leu	Asp	Asp	Gly	Tyr	Leu	Val	865	870	875	880

Gly	Ser	Arg	Gly	Ser	Val	Gly	Ser	Ser	Phe	Val	Ala	Thr	Met	Thr	Glu	
				885					890						895	
Ile	Thr	Glu	Val	Asn	Pro	Leu	Pro	Pro	His	Tyr	Val	Cys	Pro	Asn	Cys	
			900					905						910		
Lys	His	Ser	Glu	Phe	Phe	Asn	Asp	Gly	Ser	Val	Gly	Ser	Gly	Phe	Asp	
		915					920					925				
Leu	Pro	Asp	Lys	Asn	Cys	Pro	Arg	Cys	Gly	Thr	Lys	Tyr	Lys	Lys	Asp	
	930					935					940					
Gly	His	Asp	Ile	Pro	Phe	Glu	Thr	Phe	Leu	Gly	Phe	Lys	Gly	Asp	Lys	
945					950					955					960	
Val	Pro	Asp	Ile	Asp	Leu	Asn	Phe	Ser	Gly	Glu	Tyr	Gln	Pro	Arg	Ala	
			965						970						975	
His	Asn	Tyr	Thr	Lys	Val	Leu	Phe	Gly	Glu	Asp	Asn	Val	Tyr	Arg	Ala	
			980					985					990			
Gly	Thr	Ile	Gly	Thr	Val	Ala	Asp	Lys	Thr	Ala	Tyr	Gly	Phe	Val	Lys	
		995					1000					1005				
Ala	Tyr	Ala	Ser	Asp	His	Asn	Leu	Glu	Leu	Arg	Gly	Ala	Glu	Ile	Asp	
	1010					1015					1020					
Leu	Ala	Ala	Gly	Cys	Thr	Gly	Val	Lys	Arg	Thr	Thr	Gly	Gln	His	Pro	
1025					1030					1035					1040	
Gly	Gly	Ile	Ile	Val	Val	Pro	Asp	Tyr	Met	Glu	Ile	Tyr	Asp	Phe	Thr	
			1045						1050					1055		
Pro	Ile	Gln	Tyr	Pro	Ala	Asp	Asp	Thr	Ser	Ser	Glu	Trp	Arg	Thr	Thr	
			1060					1065						1070		
His	Phe	Asp	Phe	His	Ser	Ile	His	Asp	Asn	Leu	Leu	Lys	Leu	Asp	Ile	
		1075					1080					1085				
Leu	Gly	His	Asp	Asp	Pro	Thr	Val	Ile	Arg	Met	Leu	Gln	Asp	Leu	Ser	
	1090					1095					1100					
Gly	Ile	Asp	Pro	Lys	Thr	Ile	Pro	Thr	Asp	Asp	Pro	Asp	Val	Met	Gly	
1105					1110					1115					1120	
Ile	Phe	Ser	Ser	Thr	Glu	Pro	Leu	Gly	Val	Thr	Pro	Glu	Gln	Ile	Met	
				1125					1130					1135		

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val		
1140	1145	1150
Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val		
1155	1160	1165
Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala		
1170	1175	1180
Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly		
1185	1190	1200
Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro		
1205	1210	1215
Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu		
1220	1225	1230
Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp		
1235	1240	1245
Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His		
1250	1255	1260
Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val		
1265	1270	1280
His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu		
1285	1290	1295
Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys		
1300	1305	1310
Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu		
1315	1320	1325
Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg		
1330	1335	1340
Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu		
1345	1350	1360
Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro		
1365	1370	1375
Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu		
1380	1385	1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe
1425 1430

<210> 185
<211> 199
<212> PRT
<213> Thermus thermophilus

<400> 185
Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
1 5 10 15

Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser
20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
65 70 75 80

Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
85 90 95

Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
100 105 110

Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
115 120 125

Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
130 135 140

Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
145 150 155 160

Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys

165

170

175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
 180 185 190

Ala Gly Gln Pro Arg Val Asp
 195

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

gccagttacc tcgcttcct cgagggg

27

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

ggcccccttg gccttctcgg cctccat

27

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

agactcgagg ccctggagcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60
 ctggagaagg tggagaaggt ggtggccctg agggccccc tcacgggctt tgacctggtg 120
 cgctccgtcc tggagaagga cccaaggag gccctcctgc gcctcaggcg cctcaggag 180
 gagggggagg agcccctcag gctcctcggg gccctctcct ggcagttcgc cctcctcgcc 240
 cgggccttct tcctcctccg ggaaaacccc agggccaagg aggaggacct cgcccgccctc 300
 gaggcccacc cctacgccgc caagaaggcc a 331

<210> 189

<211> 110
<212> PRT
<213> Thermus thermophilus

<400> 189
Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
1 5 10 15
Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
20 25 30
Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
35 40 45
Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
50 55 60
Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
65 70 75 80
Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
85 90 95
Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
100 105 110

<210> 190
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 190
gtgggtgtcta gacatcataa cggttctggc a

31

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 191

gagggccacc accttctcca ccttctc

27

<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 192

ctccgtcctg gagaaggacc ccaag

25

<210> 193

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>

<221> primer_bind

<222> (15)

<223> S at position 15 can be either C or G

<220>

<221> primer_bind

<222> (27)

<223> S at position 27 can be either C or G

<400> 193

cgcgaattca acgcsctcct caagacsct

29

<210> 194

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 194

gacacttaac atatgggtcat cgccttcacc g

31

<210> 195
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 195
gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg

38

<210> 196
<211> 10
<212> PRT
<213> *Deinococcus radiodurans*

<400> 196
Val Ile Leu Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 197
<211> 10
<212> PRT
<213> *Methanococcus jannaschii*

<400> 197
Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 198
<211> 10
<212> PRT
<213> *Thermotoga maritima*

<400> 198
Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
1 5 10

<210> 199
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 199

ctggtgaacc cgggctccgt gggccagc

28

<210> 200

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 200

Leu	Leu	Val	Asn	Pro	Gly	Ser	Val	Gly	Gln
1				5					10

<210> 201

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 201

ctcgaggagc ttgaggaggg tggtggc

27

<210> 202

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 202

Ala	Asn	Thr	Leu	Leu	Lys	Leu	Leu	Glu
1				5				

<210> 203

<211> 32

<212> PRT

<213> *Deinococcus radiodurans*

<400> 203

Gly	Phe	Gly	Gly	Val	Gln	Leu	His	Ala	Ala	His	Gly	Tyr	Leu	Leu	Ser
1				5				10						15	

Gln	Phe	Leu	Ser	Pro	Arg	His	Asn	Val	Arg	Glu	Asp	Glu	Tyr	Gly	Gly
			20					25					30		

<210> 204

<211> 32

<212> PRT

<213> *Caenorhabditis elegans*

<400> 204

Gly	Phe	Asp	Gly	Ile	Gln	Leu	His	Gly	Ala	His	Gly	Tyr	Leu	Leu	Ser
1				5				10						15	

Gln	Phe	Thr	Ser	Pro	Thr	Thr	Asn	Lys	Arg	Val	Asp	Lys	Tyr	Gly	Gly
			20					25					30		

<210> 205

<211> 32

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 205

Gly	Phe	Ser	Gly	Val	Glu	Ile	His	Ala	Ala	His	Gly	Tyr	Leu	Leu	Ser
1				5				10						15	

Gln	Phe	Leu	Ser	Pro	Leu	Ser	Asn	Arg	Arg	Ser	Asp	Ala	Trp	Gly	Gly
			20					25					30		

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggcccacc tcctcaccga

30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr
1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtgggccc cgtggagctc cac

33

<210> 210
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: polypeptide

 <400> 210
 Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
 1 5 10

<210> 211
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

<400> 211
 ggctttccca tatggctcta caccggctc ac 32

<210> 212
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 212
 gcgtggatcc acggtcatgt ctctaagtc 29